

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Williams, James A.  
Thalley, Bruce S.
- (ii) TITLE OF INVENTION: Multivalent Vaccine For Clostridium  
Botulinum Neurotoxin
- (iii) NUMBER OF SEQUENCES: 82
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Medlen & Carroll
  - (B) STREET: 220 Montgomery Street, Suite 2200
  - (C) CITY: San Francisco
  - (D) STATE: California
  - (E) COUNTRY: United States of America
  - (F) ZIP: 94104
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Ingolia, Diane E.
  - (B) REGISTRATION NUMBER: 40,027
  - (C) REFERENCE/DOCKET NUMBER: OPHD-02304
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (415) 705-8410
  - (B) TELEFAX: (415) 397-8338

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAAATTTAG CTGCAGCATC TGAC

24

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCTAGCAAAT TCGCTTGTGT TGAA

24

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCGCATATA GCATTAGACC

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTATCTAGGC CTAAAGTAT

19

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8133 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..8130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG TCT TTA ATA TCT AAA GAA GAG TTA ATA AAA CTC GCA TAT AGC ATT  
Met Ser Leu Ile Ser Lys Glu Glu Leu Ile Lys Leu Ala Tyr Ser Ile  
1 5 10 15

48

AGA CCA AGA GAA AAT GAG TAT AAA ACT ATA CTA ACT AAT TTA GAC GAA Arg Pro Arg Glu Asn Glu Tyr Lys Thr Ile Leu Thr Asn Leu Asp Glu	96
20 25 30	
TAT AAT AAG TTA ACT ACA AAC AAT AAT GAA AAT AAA TAT TTG CAA TTA Tyr Asn Lys Leu Thr Thr Asn Asn Glu Asn Lys Tyr Leu Gln Leu	144
35 40 45	
AAA AAA CTA AAT GAA TCA ATT GAT GTT TTT ATG AAT AAA TAT AAA ACT Lys Lys Leu Asn Glu Ser Ile Asp Val Phe Met Asn Lys Tyr Lys Thr	192
50 55 60	
TCA AGC AGA AAT AGA GCA CTC TCT AAT CTA AAA AAA GAT ATA TTA AAA Ser Ser Arg Asn Arg Ala Leu Ser Asn Leu Lys Lys Asp Ile Leu Lys	240
65 70 75 80	
GAA GTA ATT CTT ATT AAA AAT TCC AAT ACA AGC CCT GTA GAA AAA AAT Glu Val Ile Leu Ile Lys Asn Ser Asn Thr Ser Pro Val Glu Lys Asn	288
85 90 95	
TTA CAT TTT GTA TGG ATA GGT GGA GAA GTC AGT GAT ATT GCT CTT GAA Leu His Phe Val Trp Ile Gly Gly Glu Val Ser Asp Ile Ala Leu Glu	336
100 105 110	
TAC ATA AAA CAA TGG GCT GAT ATT AAT GCA GAA TAT AAT ATT AAA CTG Tyr Ile Lys Gln Trp Ala Asp Ile Asn Ala Glu Tyr Asn Ile Lys Leu	384
115 120 125	
TGG TAT GAT AGT GAA GCA TTC TTA GTA AAT ACA CTA AAA AAG GCT ATA Trp Tyr Asp Ser Glu Ala Phe Leu Val Asn Thr Leu Lys Lys Ala Ile	432
130 135 140	
GTT GAA TCT TCT ACC ACT GAA GCA TTA CAG CTA CTA GAG GAA GAG ATT Val Glu Ser Ser Thr Thr Glu Ala Leu Gln Leu Leu Glu Glu Glu Ile	480
145 150 155 160	
CAA AAT CCT CAA TTT GAT AAT ATG AAA TTT TAC AAA AAA AGG ATG GAA Gln Asn Pro Gln Phe Asp Asn Met Lys Phe Tyr Lys Lys Arg Met Glu	528
165 170 175	
TTT ATA TAT GAT AGA CAA AAA AGG TTT ATA AAT TAT TAT AAA TCT CAA Phe Ile Tyr Asp Arg Gln Lys Arg Phe Ile Asn Tyr Tyr Lys Ser Gln	576
180 185 190	
ATC AAT AAA CCT ACA GTA CCT ACA ATA GAT GAT ATT ATA AAG TCT CAT Ile Asn Lys Pro Thr Val Pro Thr Ile Asp Asp Ile Ile Lys Ser His	624
195 200 205	
CTA GTA TCT GAA TAT AAT AGA GAT GAA ACT GTA TTA GAA TCA TAT AGA Leu Val Ser Glu Tyr Asn Arg Asp Glu Thr Val Leu Glu Ser Tyr Arg	672
210 215 220	
ACA AAT TCT TTG AGA AAA ATA AAT AGT AAT CAT GGG ATA GAT ATC AGG Thr Asn Ser Leu Arg Lys Ile Asn Ser Asn His Gly Ile Asp Ile Arg	720
225 230 235 240	
GCT AAT AGT TTG TTT ACA GAA CAA GAG TTA TTA AAT ATT TAT AGT CAG Ala Asn Ser Leu Phe Thr Glu Gln Glu Leu Leu Asn Ile Tyr Ser Gln	768
245 250 255	

GAG TTG TTA AAT CGT GGA AAT TTA GCT GCA GCA TCT GAC ATA GTA AGA Glu Leu Leu Asn Arg Gly Asn Leu Ala Ala Ala Ser Asp Ile Val Arg 260 265 270	816
TTA TTA GCC CTA AAA AAT TTT GGC GGA GTA TAT TTA GAT GTT GAT ATG Leu Leu Ala Leu Lys Asn Phe Gly Gly Val Tyr Leu Asp Val Asp Met 275 280 285	864
CTT CCA GGT ATT CAC TCT GAT TTA TTT AAA ACA ATA TCT AGA CCT AGC Leu Pro Gly Ile His Ser Asp Leu Phe Lys Thr Ile Ser Arg Pro Ser 290 295 300	912
TCT ATT GGA CTA GAC CGT TGG GAA ATG ATA AAA TTA GAG GCT ATT ATG Ser Ile Gly Leu Asp Arg Trp Glu Met Ile Lys Leu Glu Ala Ile Met 305 310 315 320	960
AAG TAT AAA AAA TAT ATA AAT TAT ACA TCA GAA AAC TTT GAT AAA Lys Tyr Lys Tyr Ile Asn Asn Tyr Thr Ser Glu Asn Phe Asp Lys 325 330 335	1008
CTT GAT CAA CAA TTA AAA GAT AAT TTT AAA CTC ATT ATA GAA AGT AAA Leu Asp Gln Gln Leu Lys Asp Asn Phe Lys Leu Ile Ile Glu Ser Lys 340 345 350	1056
AGT GAA AAA TCT GAG ATA TTT TCT AAA TTA GAA AAT TTA AAT GTA TCT Ser Glu Lys Ser Glu Ile Phe Ser Lys Leu Glu Asn Leu Asn Val Ser 355 360 365	1104
GAT CTT GAA ATT AAA ATA GCT TTC GCT TTA GGC AGT GTT ATA AAT CAA Asp Leu Glu Ile Lys Ile Ala Phe Ala Leu Gly Ser Val Ile Asn Gln 370 375 380	1152
GCC TTG ATA TCA AAA CAA GGT TCA TAT CTT ACT AAC CTA GTA ATA GAA Ala Leu Ile Ser Lys Gln Gly Ser Tyr Leu Thr Asn Leu Val Ile Glu 385 390 395 400	1200
CAA GTA AAA AAT AGA TAT CAA TTT TTA AAC CAA CAC CTT AAC CCA GCC Gln Val Lys Asn Arg Tyr Gln Phe Leu Asn Gin His Leu Asn Pro Ala 405 410 415	1248
ATA GAG TCT GAT AAT AAC TTC ACA GAT ACT ACT AAA ATT TTT CAT GAT Ile Glu Ser Asp Asn Asn Phe Thr Asp Thr Thr Lys Ile Phe His Asp 420 425 430	1296
TCA TTA TTT AAT TCA GCT ACC GCA GAA AAC TCT ATG TTT TTA ACA AAA Ser Leu Phe Asn Ser Ala Thr Ala Glu Asn Ser Met Phe Leu Thr Lys 435 440 445	1344
ATA GCA CCA TAC TTA CAA GTA GGT TTT ATG CCA GAA GCT CGC TCC ACA Ile Ala Pro Tyr Leu Gln Val Gly Phe Met Pro Glu Ala Arg Ser Thr 450 455 460	1392
ATA AGT TTA AGT GGT CCA GGA GCT TAT GCG TCA GCT TAC TAT GAT TTC Ile Ser Leu Ser Gly Pro Gly Ala Tyr Ala Ser Ala Tyr Tyr Asp Phe 465 470 475 480	1440
ATA AAT TTA CAA GAA AAT ACT ATA GAA AAA ACT TTA AAA GCA TCA GAT Ile Asn Leu Gln Glu Asn Thr Ile Glu Lys Thr Leu Lys Ala Ser Asp 485 490 495	1488

TTA ATA GAA TTT AAA TTC CCA GAA AAT AAT CTA TCT CAA TTG ACA GAA Leu Ile Glu Phe Lys Phe Pro Glu Asn Asn Leu Ser Gln Leu Thr Glu 500 505 510	1536
CAA GAA ATA AAT AGT CTA TGG AGC TTT GAT CAA GCA AGT GCA AAA TAT Gln Glu Ile Asn Ser Leu Trp Ser Phe Asp Gln Ala Ser Ala Lys Tyr 515 520 525	1584
CAA TTT GAG AAA TAT GTA AGA GAT TAT ACT GGT GGA TCT CTT TCT GAA Gln Phe Glu Lys Tyr Val Arg Asp Tyr Thr Gly Gly Ser Leu Ser Glu 530 535 540	1632
GAC AAT GGG GTA GAC TTT AAT AAA AAT ACT GCC CTC GAC AAA AAC TAT Asp Asn Gly Val Asp Phe Asn Lys Asn Thr Ala Leu Asp Lys Asn Tyr 545 550 555 560	1680
TTA TTA AAT AAT AAA ATT CCA TCA AAC AAT GTA GAA GAA GCT GGA AGT Leu Leu Asn Asn Lys Ile Pro Ser Asn Asn Val Glu Glu Ala Gly Ser 565 570 575	1728
AAA AAT TAT GTT CAT TAT ATC ATA CAG TTA CAA GGA GAT GAT ATA AGT Lys Asn Tyr Val His Tyr Ile Ile Gln Leu Gln Gly Asp Asp Ile Ser 580 585 590	1776
TAT GAA GCA ACA TGC AAT TTA TTT TCT AAA AAT CCT AAA AAT AGT ATT Tyr Glu Ala Thr Cys Asn Leu Phe Ser Lys Asn Pro Lys Asn Ser Ile 595 600 605	1824
ATT ATA CAA CGA AAT ATG AAT GAA AGT GCA AAA AGC TAC TTT TTA AGT Ile Ile Gln Arg Asn Met Asn Glu Ser Ala Lys Ser Tyr Phe Leu Ser 610 615 620	1872
GAT GAT GGA GAA TCT ATT TTA GAA TTA AAT AAA TAT AGG ATA CCT GAA Asp Asp Gly Glu Ser Ile Leu Glu Leu Asn Lys Tyr Arg Ile Pro Glu 625 630 635 640	1920
AGA TTA AAA AAT AAG GAA AAA GTA AAA GTA ACC TTT ATT GGA CAT GGT Arg Leu Lys Asn Lys Glu Lys Val Lys Val Thr Phe Ile Gly His Gly 645 650 655	1968
AAA GAT GAA TTC AAC ACA AGC GAA TTT GCT AGA TTA AGT GTA GAT TCA Lys Asp Glu Phe Asn Thr Ser Glu Phe Ala Arg Leu Ser Val Asp Ser 660 665 670	2016
CTT TCC AAT GAG ATA AGT TCA TTT TTA GAT ACC ATA AAA TTA GAT ATA Leu Ser Asn Glu Ile Ser Ser Phe Leu Asp Thr Ile Lys Leu Asp Ile 675 680 685	2064
TCA CCT AAA AAT GTA GAA GTA AAC TTA CTT GGA TGT AAT ATG TTT AGT Ser Pro Lys Asn Val Glu Val Asn Leu Leu Gly Cys Asn Met Phe Ser 690 695 700	2112
TAT GAT TTT AAT GTT GAA GAA ACT TAT CCT GGG AAG TTG CTA TTA AGT Tyr Asp Phe Asn Val Glu Glu Thr Tyr Pro Gly Lys Leu Leu Leu Ser 705 710 715 720	2160
ATT ATG GAC AAA ATT ACT TCC ACT TTA CCT GAT GTA AAT AAA AAT TCT Ile Met Asp Lys Ile Thr Ser Thr Leu Pro Asp Val Asn Lys Asn Ser 725 730 735	2208

ATT ACT ATA GGA GCA AAT CAA TAT GAA GTA AGA ATT AAT AGT GAG GGA Ile Thr Ile Gly Ala Asn Gln Tyr Glu Val Arg Ile Asn Ser Glu Gly 740 745 750	2256
AGA AAA GAA CTT CTG GCT CAC TCA GGT AAA TGG ATA AAT AAA GAA GAA Arg Lys Glu Leu Leu Ala His Ser Gly Lys Trp Ile Asn Lys Glu Glu 755 760 765	2304
GCT ATT ATG AGC GAT TTA TCT AGT AAA GAA TAC ATT TTT TTT GAT TCT Ala Ile Met Ser Asp Leu Ser Ser Lys Glu Tyr Ile Phe Phe Asp Ser 770 775 780	2352
ATA GAT AAT AAG CTA AAA GCA AAG TCC AAG AAT ATT CCA GGA TTA GCA Ile Asp Asn Lys Leu Lys Ala Lys Ser Lys Asn Ile Pro Gly Leu Ala 785 790 795 800	2400
TCA ATA TCA GAA GAT ATA AAA ACA TTA TTA CTT GAT GCA AGT GTT AGT Ser Ile Ser Glu Asp Ile Lys Thr Leu Leu Leu Asp Ala Ser Val Ser 805 810 815	2448
CCT GAT ACA AAA TTT ATT TTA AAT AAT CTT AAG CTT AAT ATT GAA TCT Pro Asp Thr Lys Phe Ile Leu Asn Asn Leu Lys Leu Asn Ile Glu Ser 820 825 830	2496
TCT ATT GGG GAT TAC ATT TAT TAT GAA AAA TTA GAG CCT GTT AAA AAT Ser Ile Gly Asp Tyr Ile Tyr Tyr Glu Lys Leu Glu Pro Val Lys Asn 835 840 845	2544
ATA ATT CAC AAT TCT ATA GAT GAT TTA ATA GAT GAG TTC AAT CTA CTT Ile Ile His Asn Ser Ile Asp Asp Leu Ile Asp Glu Phe Asn Leu Leu 850 855 860	2592
GAA AAT GTA TCT GAT GAA TTA TAT GAA TTA AAA AAA TTA AAT AAT CTA Glu Asn Val Ser Asp Glu Leu Tyr Glu Leu Lys Lys Leu Asn Asn Leu 865 870 875 880	2640
GAT GAG AAG TAT TTA ATA TCT TTT GAA GAT ATC TCA AAA AAT AAT TCA Asp Glu Lys Tyr Leu Ile Ser Phe Glu Asp Ile Ser Lys Asn Asn Ser 885 890 895	2688
ACT TAC TCT GTA AGA TTT ATT AAC AAA AGT AAT GGT GAG TCA GTT TAT Thr Tyr Ser Val Arg Phe Ile Asn Lys Ser Asn Gly Glu Ser Val Tyr 900 905 910	2736
GTA GAA ACA GAA AAA GAA ATT TTT TCA AAA TAT AGC GAA CAT ATT ACA Val Glu Thr Glu Lys Glu Ile Phe Ser Lys Tyr Ser Glu His Ile Thr 915 920 925	2784
AAA GAA ATA AGT ACT ATA AAG AAT AGT ATA ATT ACA GAT GTT AAT GGT Lys Glu Ile Ser Thr Ile Lys Asn Ser Ile Ile Thr Asp Val Asn Gly 930 935 940	2832
AAT TTA TTG GAT AAT ATA CAG TTA GAT CAT ACT TCT CAA GTT AAT ACA Asn Leu Leu Asp Asn Ile Gln Leu Asp His Thr Ser Gln Val Asn Thr 945 950 955 960	2880
TTA AAC GCA GCA TTC TTT ATT CAA TCA TTA ATA GAT TAT AGT AGC AAT Leu Asn Ala Ala Phe Phe Ile Gln Ser Leu Ile Asp Tyr Ser Ser Asn 965 970 975	2928

AAA GAT GTA CTG AAT GAT TTA AGT ACC TCA GTT AAG GTT CAA CTT TAT Lys Asp Val Leu Asn Asp Leu Ser Thr Ser Val Lys Val Gln Leu Tyr 980 985 990	2976
GCT CAA CTA TTT AGT ACA GGT TTA AAT ACT ATA TAT GAC TCT ATC CAA Ala Gln Leu Phe Ser Thr Gly Leu Asn Thr Ile Tyr Asp Ser Ile Gln 995 1000 1005	3024
TTA GTA AAT TTA ATA TCA AAT GCA GTA AAT GAT ACT ATA AAT GTA CTA Leu Val Asn Leu Ile Ser Asn Ala Val Asn Asp Thr Ile Asn Val Leu 1010 1015 1020	3072
CCT ACA ATA ACA GAG GGG ATA CCT ATT GTA TCT ACT ATA TTA GAC GGA Pro Thr Ile Thr Glu Gly Ile Pro Ile Val Ser Thr Ile Leu Asp Gly 1025 1030 1035 1040	3120
ATA AAC TTA GGT GCA GCA ATT AAG GAA TTA CTA GAC GAA CAT GAC CCA Ile Asn Leu Gly Ala Ala Ile Lys Glu Leu Leu Asp Glu His Asp Pro 1045 1050 1055	3168
TTA CTA AAA AAA GAA TTA GAA GCT AAG GTG GGT GTT TTA GCA ATA AAT Leu Leu Lys Glu Leu Glu Ala Lys Val Gly Val Leu Ala Ile Asn 1060 1065 1070	3216
ATG TCA TTA TCT ATA GCT GCA ACT GTA GCT TCA ATT GTT GGA ATA GGT Met Ser Leu Ser Ile Ala Ala Thr Val Ala Ser Ile Val Gly Ile Gly 1075 1080 1085	3264
GCT GAA GTT ACT ATT TTC TTA TTA CCT ATA GCT GGT ATA TCT GCA GGA Ala Glu Val Thr Ile Phe Leu Leu Pro Ile Ala Gly Ile Ser Ala Gly 1090 1095 1100	3312
ATA CCT TCA TTA GTT AAT AAT GAA TTA ATA TTG CAT GAT AAG GCA ACT Ile Pro Ser Leu Val Asn Asn Glu Leu Ile Leu His Asp Lys Ala Thr 1105 1110 1115 1120	3360
TCA GTG GTA AAC TAT TTT AAT CAT TTG TCT GAA TCT AAA AAA TAT GGC Ser Val Val Asn Tyr Phe Asn His Leu Ser Glu Ser Lys Lys Tyr Gly 1125 1130 1135	3408
CCT CTT AAA ACA GAA GAT GAT AAA ATT TTA GTT CCT ATT GAT GAT TTA Pro Leu Lys Thr Glu Asp Asp Lys Ile Leu Val Pro Ile Asp Asp Leu 1140 1145 1150	3456
GTA ATA TCA GAA ATA GAT TTT AAT AAT AAT TCG ATA AAA CTA GGA ACA Val Ile Ser Glu Ile Asp Phe Asn Asn Asn Ser Ile Lys Leu Gly Thr 1155 1160 1165	3504
TGT AAT ATA TTA GCA ATG GAG GGG GGA TCA GGA CAC ACA GTG ACT GGT Cys Asn Ile Leu Ala Met Glu Gly Gly Ser Gly His Thr Val Thr Gly 1170 1175 1180	3552
AAT ATA GAT CAC TTT TTC TCA TCT CCA TCT ATA AGT TCT CAT ATT CCT Asn Ile Asp His Phe Phe Ser Ser Pro Ser Ile Ser Ser His Ile Pro 1185 1190 1195 1200	3600
TCA TTA TCA ATT TAT TCT GCA ATA GGT ATA GAA ACA GAA AAT CTA GAT Ser Leu Ser Ile Tyr Ser Ala Ile Gly Ile Glu Thr Glu Asn Leu Asp 1205 1210 1215	3648

TTT TCA AAA AAA ATA ATG ATG TTA CCT AAT GCT CCT TCA AGA GTG TTT Phe Ser Lys Lys Ile Met Met Leu Pro Asn Ala Pro Ser Arg Val Phe 1220 1225 1230	3696
TGG TGG GAA ACT GGA GCA GTT CCA GGT TTA AGA TCA TTG GAA AAT GAC Trp Trp Glu Thr Gly Ala Val Pro Gly Leu Arg Ser Leu Glu Asn Asp 1235 1240 1245	3744
GGA ACT AGA TTA CTT GAT TCA ATA AGA GAT TTA TAC CCA GGT AAA TTT Gly Thr Arg Leu Leu Asp Ser Ile Arg Asp Leu Tyr Pro Gly Lys Phe 1250 1255 1260	3792
TAC TGG AGA TTC TAT GCT TTT TTC GAT TAT GCA ATA ACT ACA TTA AAA Tyr Trp Arg Phe Tyr Ala Phe Phe Asp Tyr Ala Ile Thr Thr Leu Lys 1265 1270 1275 1280	3840
CCA GTT TAT GAA GAC ACT AAT ATT AAA ATT AAA CTA GAT AAA GAT ACT Pro Val Tyr Glu Asp Thr Asn Ile Lys Ile Lys Leu Asp Lys Asp Thr 1285 1290 1295	3888
AGA AAC TTC ATA ATG CCA ACT ATA ACT ACT AAC GAA ATT AGA AAC AAA Arg Asn Phe Ile Met Pro Thr Ile Thr Thr Asn Glu Ile Arg Asn Lys 1300 1305 1310	3936
TTA TCT TAT TCA TTT GAT GGA GCA GGA GGA ACT TAC TCT TTA TTA TTA Leu Ser Tyr Ser Phe Asp Gly Ala Gly Gly Thr Tyr Ser Leu Leu Leu 1315 1320 1325	3984
TCT TCA TAT CCA ATA TCA ACG AAT ATA AAT TTA TCT AAA GAT GAT TTA Ser Ser Tyr Pro Ile Ser Thr Asn Ile Asn Leu Ser Lys Asp Asp Leu 1330 1335 1340	4032
TGG ATA TTT AAT ATT GAT AAT GAA GTA AGA GAA ATA TCT ATA GAA AAT Trp Ile Phe Asn Ile Asp Asn Glu Val Arg Glu Ile Ser Ile Glu Asn 1345 1350 1355 1360	4080
GGT ACT ATT AAA AAA GGA AAG TTA ATA AAA GAT GTT TTA AGT AAA ATT Gly Thr Ile Lys Lys Gly Lys Leu Ile Lys Asp Val Leu Ser Lys Ile 1365 1370 1375	4128
GAT ATA AAT AAA AAT AAA CTT ATT ATA GGC AAT CAA ACA ATA GAT TTT Asp Ile Asn Lys Asn Lys Leu Ile Ile Gly Asn Gln Thr Ile Asp Phe 1380 1385 1390	4176
TCA GGC GAT ATA GAT AAT AAA GAT AGA TAT ATA TTC TTG ACT TGT GAG Ser Gly Asp Ile Asp Asn Lys Asp Arg Tyr Ile Phe Leu Thr Cys Glu 1395 1400 1405	4224
TTA GAT GAT AAA ATT AGT TTA ATA ATA GAA ATA AAT CTT GTT GCA AAA Leu Asp Asp Lys Ile Ser Leu Ile Ile Glu Ile Asn Leu Val Ala Lys 1410 1415 1420	4272
TCT TAT AGT TTG TTA TTG TCT GGG GAT AAA AAT TAT TTG ATA TCC AAT Ser Tyr Ser Leu Leu Ser Gly Asp Lys Asn Tyr Leu Ile Ser Asn 1425 1430 1435 1440	4320
TTA TCT AAT ACT ATT GAG AAA ATC AAT ACT TTA GGC CTA GAT AGT AAA Leu Ser Asn Thr Ile Glu Lys Ile Asn Thr Leu Gly Leu Asp Ser Lys 1445 1450 1455	4368

AAT ATA GCG TAC AAT TAC ACT GAT GAA TCT AAT AAA TAT TTT GGA Asn Ile Ala Tyr Asn Tyr Thr Asp Glu Ser Asn Asn Lys Tyr Phe Gly 1460 1465 1470	4416
GCT ATA TCT AAA ACA AGT CAA AAA AGC ATA ATA CAT TAT AAA AAA GAC Ala Ile Ser Lys Thr Ser Gln Lys Ser Ile Ile His Tyr Lys Lys Asp 1475 1480 1485	4464
AGT AAA AAT ATA TTA GAA TTT TAT AAT GAC AGT ACA TTA GAA TTT AAC Ser Lys Asn Ile Leu Glu Phe Tyr Asn Asp Ser Thr Leu Glu Phe Asn 1490 1495 1500	4512
AGT AAA GAT TTT ATT GCT GAA GAT ATA AAT GTA TTT ATG AAA GAT GAT Ser Lys Asp Phe Ile Ala Glu Asp Ile Asn Val Phe Met Lys Asp Asp 1505 1510 1515 1520	4560
ATT AAT ACT ATA ACA GGA AAA TAC TAT GTT GAT AAT AAT ACT GAT AAA Ile Asn Thr Ile Thr Gly Lys Tyr Tyr Val Asp Asn Asn Thr Asp Lys 1525 1530 1535	4608
AGT ATA GAT TTC TCT ATT TCT TTA GTT AGT AAA AAT CAA GTA AAA GTA Ser Ile Asp Phe Ser Ile Ser Leu Val Ser Lys Asn Gln Val Lys Val 1540 1545 1550	4656
AAT GGA TTA TAT TTA AAT GAA TCC GTA TAC TCA TCT TAC CTT GAT TTT Asn Gly Leu Tyr Leu Asn Glu Ser Val Tyr Ser Ser Tyr Leu Asp Phe 1555 1560 1565	4704
GTG AAA AAT TCA GAT GGA CAC CAT AAT ACT TCT AAT TTT ATG AAT TTA Val Lys Asn Ser Asp Gly His His Asn Thr Ser Asn Phe Met Asn Leu 1570 1575 1580	4752
TTT TTG GAC AAT ATA AGT TTC TGG AAA TTG TTT GGG TTT GAA AAT ATA Phe Leu Asp Asn Ile Ser Phe Trp Lys Leu Phe Gly Phe Glu Asn Ile 1585 1590 1595 1600	4800
AAT TTT GTA ATC GAT AAA TAC TTT ACC CTT GTT GGT AAA ACT AAT CTT Asn Phe Val Ile Asp Lys Tyr Phe Thr Leu Val Gly Lys Thr Asn Leu 1605 1610 1615	4848
GGA TAT GTA GAA TTT ATT TGT GAC AAT AAT AAA AAT ATA GAT ATA TAT Gly Tyr Val Glu Phe Ile Cys Asp Asn Asn Lys Asn Ile Asp Ile Tyr 1620 1625 1630	4896
TTT GGT GAA TGG AAA ACA TCG TCA TCT AAA AGC ACT ATA TTT AGC GGA Phe Gly Glu Trp Lys Thr Ser Ser Ser Lys Ser Thr Ile Phe Ser Gly 1635 1640 1645	4944
AAT GGT AGA AAT GTT GTA GTC GAG CCT ATA TAT AAT CCT GAT ACG GGT Asn Gly Arg Asn Val Val Glu Pro Ile Tyr Asn Pro Asp Thr Gly 1650 1655 1660	4992
GAA GAT ATA TCT ACT TCA CTA GAT TTT TCC TAT GAA CCT CTC TAT GGA Glu Asp Ile Ser Thr Ser Leu Asp Phe Ser Tyr Glu Pro Leu Tyr Gly 1665 1670 1675 1680	5040
ATA GAT AGA TAT ATA AAT AAA GTA TTG ATA GCA CCT GAT TTA TAT ACA Ile Asp Arg Tyr Ile Asn Lys Val Leu Ile Ala Pro Asp Leu Tyr Thr 1685 1690 1695	5088

AGT TTA ATA AAT ATT AAT ACC AAT TAT TAT TCA AAT GAG TAC TAC CCT Ser Leu Ile Asn Ile Asn Thr Asn Tyr Tyr Ser Asn Glu Tyr Tyr Pro 1700 1705 1710	5136
GAG ATT ATA GTT CTT AAC CCA AAT ACA TTC CAC AAA AAA GTA AAT ATA Glu Ile Ile Val Leu Asn Pro Asn Thr Phe His Lys Lys Val Asn Ile 1715 1720 1725	5184
AAT TTA GAT AGT TCT TCT TTT GAG TAT AAA TGG TCT ACA GAA GGA AGT Asn Leu Asp Ser Ser Phe Glu Tyr Lys Trp Ser Thr Glu Gly Ser 1730 1735 1740	5232
GAC TTT ATT TTA GTT AGA TAC TTA GAA GAA AGT AAT AAA AAA ATA TTA Asp Phe Ile Leu Val Arg Tyr Leu Glu Glu Ser Asn Lys Lys Ile Leu 1745 1750 1755 1760	5280
CAA AAA ATA AGA ATC AAA GGT ATC TTA TCT AAT ACT CAA TCA TTT AAT Gln Lys Ile Arg Ile Lys Gly Ile Leu Ser Asn Thr Gln Ser Phe Asn 1765 1770 1775	5328
AAA ATG AGT ATA GAT TTT AAA GAT ATT AAA AAA CTA TCA TTA GGA TAT Lys Met Ser Ile Asp Phe Lys Asp Ile Lys Lys Leu Ser Leu Gly Tyr 1780 1785 1790	5376
ATA ATG AGT AAT TTT AAA TCA TTT AAT TCT GAA AAT GAA TTA GAT AGA Ile Met Ser Asn Phe Lys Ser Phe Asn Ser Glu Asn Glu Leu Asp Arg 1795 1800 1805	5424
GAT CAT TTA GGA TTT AAA ATA ATA GAT AAT AAA ACT TAT TAC TAT GAT Asp His Leu Gly Phe Lys Ile Ile Asp Asn Lys Thr Tyr Tyr Tyr Asp 1810 1815 1820	5472
GAA GAT AGT AAA TTA GTT AAA GGA TTA ATC AAT ATA AAT AAT TCA TTA Glu Asp Ser Lys Leu Val Lys Gly Leu Ile Asn Ile Asn Asn Ser Leu 1825 1830 1835 1840	5520
TTC TAT TTT GAT CCT ATA GAA TTT AAC TTA GTA ACT GGA TGG CAA ACT Phe Tyr Phe Asp Pro Ile Glu Phe Asn Leu Val Thr Gly Trp Gln Thr 1845 1850 1855	5568
ATC AAT GGT AAA AAA TAT TAT TTT GAT ATA AAT ACT GGA GCA GCT TTA Ile Asn Gly Lys Tyr Tyr Phe Asp Ile Asn Thr Gly Ala Ala Leu 1860 1865 1870	5616
ACT AGT TAT AAA ATT ATT AAT GGT AAA CAC TTT TAT TTT AAT AAT GAT Thr Ser Tyr Lys Ile Ile Asn Gly Lys His Phe Tyr Phe Asn Asn Asp 1875 1880 1885	5664
GGT GTG ATG CAG TTG GGA GTA TTT AAA GGA CCT GAT GGA TTT GAA TAT Gly Val Met Gln Leu Gly Val Phe Lys Gly Pro Asp Gly Phe Glu Tyr 1890 1895 1900	5712
TTT GCA CCT GCC AAT ACT CAA AAT AAT AAC ATA GAA GGT CAG GCT ATA Phe Ala Pro Ala Asn Thr Gln Asn Asn Asn Ile Glu Gly Gln Ala Ile 1905 1910 1915 1920	5760
GTT TAT CAA AGT AAA TTC TTA ACT TTG AAT GGC AAA AAA TAT TAT TTT Val Tyr Gln Ser Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe 1925 1930 1935	5808

GAT AAT AAC TCA AAA GCA GTC ACT GGA TGG AGA ATT ATT AAC AAT GAG Asp Asn Asn Ser Lys Ala Val Thr Gly Trp Arg Ile Ile Asn Asn Glu 1940 1945 1950	5856
AAA TAT TAC TTT AAT CCT AAT AAT GCT ATT GCT GCA GTC GGA TTG CAA Lys Tyr Tyr Phe Asn Pro Asn Ala Ile Ala Ala Val Gly Leu Gln 1955 1960 1965	5904
GTA ATT GAC AAT AAT AAG TAT TAT TTC AAT CCT GAC ACT GCT ATC ATC Val Ile Asp Asn Asn Lys Tyr Tyr Phe Asn Pro Asp Thr Ala Ile Ile 1970 1975 1980	5952
TCA AAA GGT TGG CAG ACT GTT AAT GGT AGT AGA TAC TAC TTT GAT ACT Ser Lys Gly Trp Gln Thr Val Asn Gly Ser Arg Tyr Tyr Phe Asp Thr 1985 1990 1995 2000	6000
GAT ACC GCT ATT GCC TTT AAT GGT TAT AAA ACT ATT GAT GGT AAA CAC Asp Thr Ala Ile Ala Phe Asn Gly Tyr Lys Thr Ile Asp Gly Lys His 2005 2010 2015	6048
TTT TAT TTT GAT AGT GAT TGT GTA GTG AAA ATA GGT GTG TTT AGT ACC Phe Tyr Phe Asp Ser Asp Cys Val Val Lys Ile Gly Val Phe Ser Thr 2020 2025 2030	6096
TCT AAT GGA TTT GAA TAT TTT GCA CCT GCT AAT ACT TAT AAT AAT AAC Ser Asn Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Tyr Asn Asn Asn 2035 2040 2045	6144
ATA GAA GGT CAG GCT ATA GTT TAT CAA AGT AAA TTC TTA ACT TTG AAT Ile Glu Gly Gln Ala Ile Val Tyr Gln Ser Lys Phe Leu Thr Leu Asn 2050 2055 2060	6192
GGT AAA AAA TAT TAC TTT GAT AAT AAC TCA AAA GCA GTT ACC GGA TTG Gly Lys Lys Tyr Tyr Phe Asp Asn Asn Ser Lys Ala Val Thr Gly Leu 2065 2070 2075 2080	6240
CAA ACT ATT GAT AGT AAA AAA TAT TAC TTT AAT ACT AAC ACT GCT GAA Gln Thr Ile Asp Ser Lys Tyr Tyr Phe Asn Thr Asn Thr Ala Glu 2085 2090 2095	6288
GCA GCT ACT GGA TGG CAA ACT ATT GAT GGT AAA AAA TAT TAC TTT AAT Ala Ala Thr Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn 2100 2105 2110	6336
ACT AAC ACT GCT GAA GCA GCT ACT GGA TGG CAA ACT ATT GAT GGT AAA Thr Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile Asp Gly Lys 2115 2120 2125	6384
AAA TAT TAC TTT AAT ACT AAC ACT GCT ATA GCT TCA ACT GGT TAT ACA Lys Tyr Tyr Phe Asn Thr Asn Thr Ala Ile Ala Ser Thr Gly Tyr Thr 2130 2135 2140	6432
ATT ATT AAT GGT AAA CAT TTT TAT TTT AAT ACT GAT GGT ATT ATG CAG Ile Ile Asn Gly Lys His Phe Tyr Phe Asn Thr Asp Gly Ile Met Gln 2145 2150 2155 2160	6480
ATA GGA GTG TTT AAA GGA CCT AAT GGA TTT GAA TAT TTT GCA CCT GCT Ile Gly Val Phe Lys Gly Pro Asn Gly Phe Glu Tyr Phe Ala Pro Ala 2165 2170 2175	6528

AAT ACG GAT GCT AAC AAC ATA GAA GGT CAA GCT ATA CTT TAC CAA AAT Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile Leu Tyr Gln Asn 2180 2185 2190	6576
GAA TTC TTA ACT TTG AAT GGT AAA AAA TAT TAC TTT GGT AGT GAC TCA Glu Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Gly Ser Asp Ser 2195 2200 2205	6624
AAA GCA GTT ACT GGA TGG AGA ATT ATT AAC AAT AAG AAA TAT TAC TTT Lys Ala Val Thr Gly Trp Arg Ile Ile Asn Asn Lys Lys Tyr Tyr Phe 2210 2215 2220	6672
AAT CCT AAT AAT GCT ATT GCT GCA ATT CAT CTA TGC ACT ATA AAT AAT Asn Pro Asn Asn Ala Ile Ala Ile His Leu Cys Thr Ile Asn Asn 2225 2230 2235 2240	6720
GAC AAG TAT TAC TTT AGT TAT GAT GGA ATT CTT CAA AAT GGA TAT ATT Asp Lys Tyr Tyr Phe Ser Tyr Asp Gly Ile Leu Gln Asn Gly Tyr Ile 2245 2250 2255	6768
ACT ATT GAA AGA AAT AAT TTC TAT TTT GAT GCT AAT AAT GAA TCT AAA Thr Ile Glu Arg Asn Asn Phe Tyr Phe Asp Ala Asn Asn Glu Ser Lys 2260 2265 2270	6816
ATG GTA ACA GGA GTA TTT AAA GGA CCT AAT GGA TTT GAG TAT TTT GCA Met Val Thr Gly Val Phe Lys Gly Pro Asn Gly Phe Glu Tyr Phe Ala 2275 2280 2285	6864
CCT GCT AAT ACT CAC AAT AAT AAC ATA GAA GGT CAG GCT ATA GTT TAC Pro Ala Asn Thr His Asn Asn Ile Glu Gly Gln Ala Ile Val Tyr 2290 2295 2300	6912
CAG AAC AAA TTC TTA ACT TTG AAT GGC AAA AAA TAT TAT TTT GAT AAT Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys Tyr Tyr Phe Asp Asn 2305 2310 2315 2320	6960
GAC TCA AAA GCA GTT ACT GGA TGG CAA ACC ATT GAT GGT AAA AAA TAT Asp Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr 2325 2330 2335	7008
TAC TTT AAT CTT AAC ACT GCT GAA GCA GCT ACT GGA TGG CAA ACT ATT Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile 2340 2345 2350	7056
GAT GGT AAA AAA TAT TAC TTT AAT CTT AAC ACT GCT GAA GCA GCT ACT Asp Gly Lys Lys Tyr Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr 2355 2360 2365	7104
GGA TGG CAA ACT ATT GAT GGT AAA AAA TAT TAC TTT AAT ACT AAC ACT Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr 2370 2375 2380	7152
TTC ATA GCC TCA ACT GGT TAT ACA AGT ATT AAT GGT AAA CAT TTT TAT Phe Ile Ala Ser Thr Gly Tyr Thr Ser Ile Asn Gly Lys His Phe Tyr 2385 2390 2395 2400	7200
TTT AAT ACT GAT GGT ATT ATG CAG ATA GGA GTG TTT AAA GGA CCT AAT Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro Asn 2405 2410 2415	7248

GGA TTT GAA TAC TTT GCA CCT GCT AAT ACG GAT GCT AAC AAC ATA GAA Gly Phe Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu 2420 2425 2430	7296
GGT CAA GCT ATA CTT TAC CAA AAT AAA TTC TTA ACT TTG AAT GGT AAA Gly Gln Ala Ile Leu Tyr Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys 2435 2440 2445	7344
AAA TAT TAC TTT GGT AGT GAC TCA AAA GCA GTT ACC GGA CTG CGA ACT Lys Tyr Tyr Phe Gly Ser Asp Ser Lys Ala Val Thr Gly Leu Arg Thr 2450 2455 2460	7392
ATT GAT GGT AAA AAA TAT TAC TTT AAT ACT AAC ACT GCT GTT GCA GTT Ile Asp Gly Lys Tyr Tyr Phe Asn Thr Asn Thr Ala Val Ala Val 2465 2470 2475 2480	7440
ACT GGA TGG CAA ACT ATT AAT GGT AAA AAA TAC TAC TTT AAT ACT AAC Thr Gly Trp Gln Thr Ile Asn Gly Lys Tyr Tyr Phe Asn Thr Asn 2485 2490 2495	7488
ACT TCT ATA GCT TCA ACT GGT TAT ACA ATT ATT AGT GGT AAA CAT TTT Thr Ser Ile Ala Ser Thr Gly Tyr Thr Ile Ile Ser Gly Lys His Phe 2500 2505 2510	7536
TAT TTT AAT ACT GAT GGT ATT ATG CAG ATA GGA GTG TTT AAA GGA CCT Tyr Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro 2515 2520 2525	7584
GAT GGA TTT GAA TAC TTT GCA CCT GCT AAT ACA GAT GCT AAC AAT ATA Asp Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile 2530 2535 2540	7632
GAA GGT CAA GCT ATA CGT TAT CAA AAT AGA TTC CTA TAT TTA CAT GAC Glu Gly Gln Ala Ile Arg Tyr Gln Asn Arg Phe Leu Tyr Leu His Asp 2545 2550 2555 2560	7680
AAT ATA TAT TAT TTT GGT AAT AAT TCA AAA GCG GCT ACT GGT TGG GTA Asn Ile Tyr Tyr Phe Gly Asn Asn Ser Lys Ala Ala Thr Gly Trp Val 2565 2570 2575	7728
ACT ATT GAT GGT AAT AGA TAT TAC TTC GAG CCT AAT ACA GCT ATG GGT Thr Ile Asp Gly Asn Arg Tyr Tyr Phe Glu Pro Asn Thr Ala Met Gly 2580 2585 2590	7776
GCG AAT GGT TAT AAA ACT ATT GAT AAT AAA AAT TTT TAC TTT AGA AAT Ala Asn Gly Tyr Lys Thr Ile Asp Asn Lys Asn Phe Tyr Phe Arg Asn 2595 2600 2605	7824
GGT TTA CCT CAG ATA GGA GTG TTT AAA GGG TCT AAT GGA TTT GAA TAC Gly Leu Pro Gln Ile Gly Val Phe Lys Gly Ser Asn Gly Phe Glu Tyr 2610 2615 2620	7872
TTT GCA CCT GCT AAT ACG GAT GCT AAC AAT ATA GAA GGT CAA GCT ATA Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile 2625 2630 2635 2640	7920
CGT TAT CAA AAT AGA TTC CTA CAT TTA CTT GGA AAA ATA TAT TAC TTT Arg Tyr Gln Asn Arg Phe Leu His Leu Leu Gly Lys Ile Tyr Tyr Phe 2645 2650 2655	7968

GGT AAT AAT TCA AAA GCA GTT ACT GGA TGG CAA ACT ATT AAT GGT AAA	8016
Gly Asn Asn Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asn Gly Lys	
2660 2665 2670	
GTA TAT TAC TTT ATG CCT GAT ACT GCT ATG GCT GCA GCT GGT GGA CTT	8064
Val Tyr Tyr Phe Met Pro Asp Thr Ala Met Ala Ala Gly Gly Leu	
2675 2680 2685	
TTC GAG ATT GAT GGT GTT ATA TAT TTC TTT GGT GTT GAT GGA GTA AAA	8112
Phe Glu Ile Asp Gly Val Ile Tyr Phe Phe Gly Val Asp Gly Val Lys	
2690 2695 2700	
GCC CCT GGG ATA TAT GGC TAA	8133
Ala Pro Gly Ile Tyr Gly	
2705 2710	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2710 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Leu Ile Ser Lys Glu Glu Leu Ile Lys Leu Ala Tyr Ser Ile	
1 5 10 15	
Arg Pro Arg Glu Asn Glu Tyr Lys Thr Ile Leu Thr Asn Leu Asp Glu	
20 25 30	
Tyr Asn Lys Leu Thr Thr Asn Asn Asn Glu Asn Lys Tyr Leu Gln Leu	
35 40 45	
Lys Lys Leu Asn Glu Ser Ile Asp Val Phe Met Asn Lys Tyr Lys Thr	
50 55 60	
Ser Ser Arg Asn Arg Ala Leu Ser Asn Leu Lys Lys Asp Ile Leu Lys	
65 70 75 80	
Glu Val Ile Leu Ile Lys Asn Ser Asn Thr Ser Pro Val Glu Lys Asn	
85 90 95	
Leu His Phe Val Trp Ile Gly Gly Glu Val Ser Asp Ile Ala Leu Glu	
100 105 110	
Tyr Ile Lys Gln Trp Ala Asp Ile Asn Ala Glu Tyr Asn Ile Lys Leu	
115 120 125	
Trp Tyr Asp Ser Glu Ala Phe Leu Val Asn Thr Leu Lys Lys Ala Ile	
130 135 140	
Val Glu Ser Ser Thr Thr Glu Ala Leu Gln Leu Leu Glu Glu Ile	
145 150 155 160	
Gln Asn Pro Gln Phe Asp Asn Met Lys Phe Tyr Lys Lys Arg Met Glu	
165 170 175	
Phe Ile Tyr Asp Arg Gln Lys Arg Phe Ile Asn Tyr Tyr Lys Ser Gln	
180 185 190	

Ile Asn Lys Pro Thr Val Pro Thr Ile Asp Asp Ile Ile Lys Ser His  
 195 200 205  
 Leu Val Ser Glu Tyr Asn Arg Asp Glu Thr Val Leu Glu Ser Tyr Arg  
 210 215 220  
 Thr Asn Ser Leu Arg Lys Ile Asn Ser Asn His Gly Ile Asp Ile Arg  
 225 230 235 240  
 Ala Asn Ser Leu Phe Thr Glu Gln Glu Leu Leu Asn Ile Tyr Ser Gln  
 245 250 255  
 Glu Leu Leu Asn Arg Gly Asn Leu Ala Ala Ala Ser Asp Ile Val Arg  
 260 265 270  
 Leu Leu Ala Leu Lys Asn Phe Gly Gly Val Tyr Leu Asp Val Asp Met  
 275 280 285  
 Leu Pro Gly Ile His Ser Asp Leu Phe Lys Thr Ile Ser Arg Pro Ser  
 290 295 300  
 Ser Ile Gly Leu Asp Arg Trp Glu Met Ile Lys Leu Glu Ala Ile Met  
 305 310 315 320  
 Lys Tyr Lys Lys Tyr Ile Asn Asn Tyr Thr Ser Glu Asn Phe Asp Lys  
 325 330 335  
 Leu Asp Gln Gln Leu Lys Asp Asn Phe Lys Leu Ile Ile Glu Ser Lys  
 340 345 350  
 Ser Glu Lys Ser Glu Ile Phe Ser Lys Leu Glu Asn Leu Asn Val Ser  
 355 360 365  
 Asp Leu Glu Ile Lys Ile Ala Phe Ala Leu Gly Ser Val Ile Asn Gln  
 370 375 380  
 Ala Leu Ile Ser Lys Gln Gly Ser Tyr Leu Thr Asn Leu Val Ile Glu  
 385 390 395 400  
 Gln Val Lys Asn Arg Tyr Gln Phe Leu Asn Gln His Leu Asn Pro Ala  
 405 410 415  
 Ile Glu Ser Asp Asn Asn Phe Thr Asp Thr Thr Lys Ile Phe His Asp  
 420 425 430  
 Ser Leu Phe Asn Ser Ala Thr Ala Glu Asn Ser Met Phe Leu Thr Lys  
 435 440 445  
 Ile Ala Pro Tyr Leu Gln Val Gly Phe Met Pro Glu Ala Arg Ser Thr  
 450 455 460  
 Ile Ser Leu Ser Gly Pro Gly Ala Tyr Ala Ser Ala Tyr Tyr Asp Phe  
 465 470 475 480  
 Ile Asn Leu Gln Glu Asn Thr Ile Glu Lys Thr Leu Lys Ala Ser Asp  
 485 490 495  
 Leu Ile Glu Phe Lys Phe Pro Glu Asn Asn Leu Ser Gln Leu Thr Glu  
 500 505 510  
 Gln Glu Ile Asn Ser Leu Trp Ser Phe Asp Gln Ala Ser Ala Lys Tyr  
 515 520 525

Gln Phe Glu Lys Tyr Val Arg Asp Tyr Thr Gly Gly Ser Leu Ser Glu  
530 535 540

Asp Asn Gly Val Asp Phe Asn Lys Asn Thr Ala Leu Asp Lys Asn Tyr  
545 550 555 560

Leu Leu Asn Asn Lys Ile Pro Ser Asn Asn Val Glu Glu Ala Gly Ser  
565 570 575

Lys Asn Tyr Val His Tyr Ile Ile Gln Leu Gln Gly Asp Asp Ile Ser  
580 585 590

Tyr Glu Ala Thr Cys Asn Leu Phe Ser Lys Asn Pro Lys Asn Ser Ile  
595 600 605

Ile Ile Gln Arg Asn Met Asn Glu Ser Ala Lys Ser Tyr Phe Leu Ser  
610 615 620

Asp Asp Gly Glu Ser Ile Leu Glu Leu Asn Lys Tyr Arg Ile Pro Glu  
625 630 635 640

Arg Leu Lys Asn Lys Glu Lys Val Lys Val Thr Phe Ile Gly His Gly  
645 650 655

Lys Asp Glu Phe Asn Thr Ser Glu Phe Ala Arg Leu Ser Val Asp Ser  
660 665 670

Leu Ser Asn Glu Ile Ser Ser Phe Leu Asp Thr Ile Lys Leu Asp Ile  
675 680 685

Ser Pro Lys Asn Val Glu Val Asn Leu Leu Gly Cys Asn Met Phe Ser  
690 695 700

Tyr Asp Phe Asn Val Glu Glu Thr Tyr Pro Gly Lys Leu Leu Leu Ser  
705 710 715 720

Ile Met Asp Lys Ile Thr Ser Thr Leu Pro Asp Val Asn Lys Asn Ser  
725 730 735

Ile Thr Ile Gly Ala Asn Gln Tyr Glu Val Arg Ile Asn Ser Glu Gly  
740 745 750

Arg Lys Glu Leu Leu Ala His Ser Gly Lys Trp Ile Asn Lys Glu Glu  
755 760 765

Ala Ile Met Ser Asp Leu Ser Ser Lys Glu Tyr Ile Phe Phe Asp Ser  
770 775 780

Ile Asp Asn Lys Leu Lys Ala Lys Ser Lys Asn Ile Pro Gly Leu Ala  
785 790 795 800

Ser Ile Ser Glu Asp Ile Lys Thr Leu Leu Leu Asp Ala Ser Val Ser  
805 810 815

Pro Asp Thr Lys Phe Ile Leu Asn Asn Leu Lys Leu Asn Ile Glu Ser  
820 825 830

Ser Ile Gly Asp Tyr Ile Tyr Tyr Glu Lys Leu Glu Pro Val Lys Asn  
835 840 845

Ile Ile His Asn Ser Ile Asp Asp Leu Ile Asp Glu Phe Asn Leu Leu  
850 855 860

Glu Asn Val Ser Asp Glu Leu Tyr Glu Leu Lys Lys Leu Asn Asn Leu  
 865 870 875 880  
 Asp Glu Lys Tyr Leu Ile Ser Phe Glu Asp Ile Ser Lys Asn Asn Ser  
 885 890 895  
 Thr Tyr Ser Val Arg Phe Ile Asn Lys Ser Asn Gly Glu Ser Val Tyr  
 900 905 910  
 Val Glu Thr Glu Lys Glu Ile Phe Ser Lys Tyr Ser Glu His Ile Thr  
 915 920 925  
 Lys Glu Ile Ser Thr Ile Lys Asn Ser Ile Ile Thr Asp Val Asn Gly  
 930 935 940  
 Asn Leu Leu Asp Asn Ile Gln Leu Asp His Thr Ser Gln Val Asn Thr  
 945 950 955 960  
 Leu Asn Ala Ala Phe Phe Ile Gln Ser Leu Ile Asp Tyr Ser Ser Asn  
 965 970 975  
 Lys Asp Val Leu Asn Asp Leu Ser Thr Ser Val Lys Val Gln Leu Tyr  
 980 985 990  
 Ala Gln Leu Phe Ser Thr Gly Leu Asn Thr Ile Tyr Asp Ser Ile Gln  
 995 1000 1005  
 Leu Val Asn Leu Ile Ser Asn Ala Val Asn Asp Thr Ile Asn Val Leu  
 1010 1015 1020  
 Pro Thr Ile Thr Glu Gly Ile Pro Ile Val Ser Thr Ile Leu Asp Gly  
 1025 1030 1035 1040  
 Ile Asn Leu Gly Ala Ala Ile Lys Glu Leu Leu Asp Glu His Asp Pro  
 1045 1050 1055  
 Leu Leu Lys Lys Glu Leu Glu Ala Lys Val Gly Val Leu Ala Ile Asn  
 1060 1065 1070  
 Met Ser Leu Ser Ile Ala Ala Thr Val Ala Ser Ile Val Gly Ile Gly  
 1075 1080 1085  
 Ala Glu Val Thr Ile Phe Leu Leu Pro Ile Ala Gly Ile Ser Ala Gly  
 1090 1095 1100  
 Ile Pro Ser Leu Val Asn Asn Glu Leu Ile Leu His Asp Lys Ala Thr  
 1105 1110 1115 1120  
 Ser Val Val Asn Tyr Phe Asn His Leu Ser Glu Ser Lys Lys Tyr Gly  
 1125 1130 1135  
 Pro Leu Lys Thr Glu Asp Asp Lys Ile Leu Val Pro Ile Asp Asp Leu  
 1140 1145 1150  
 Val Ile Ser Glu Ile Asp Phe Asn Asn Asn Ser Ile Lys Leu Gly Thr  
 1155 1160 1165  
 Cys Asn Ile Leu Ala Met Glu Gly Gly Ser Gly His Thr Val Thr Gly  
 1170 1175 1180  
 Asn Ile Asp His Phe Phe Ser Ser Pro Ser Ile Ser Ser His Ile Pro  
 1185 1190 1195 1200

Ser Leu Ser Ile Tyr Ser Ala Ile Gly Ile Glu Thr Glu Asn Leu Asp  
1205 1210 1215

Phe Ser Lys Lys Ile Met Met Leu Pro Asn Ala Pro Ser Arg Val Phe  
1220 1225 1230

Trp Trp Glu Thr Gly Ala Val Pro Gly Leu Arg Ser Leu Glu Asn Asp  
1235 1240 1245

Gly Thr Arg Leu Leu Asp Ser Ile Arg Asp Leu Tyr Pro Gly Lys Phe  
1250 1255 1260

Tyr Trp Arg Phe Tyr Ala Phe Phe Asp Tyr Ala Ile Thr Thr Leu Lys  
1265 1270 1275 1280

Pro Val Tyr Glu Asp Thr Asn Ile Lys Ile Lys Leu Asp Lys Asp Thr  
1285 1290 1295

Arg Asn Phe Ile Met Pro Thr Ile Thr Thr Asn Glu Ile Arg Asn Lys  
1300 1305 1310

Leu Ser Tyr Ser Phe Asp Gly Ala Gly Gly Thr Tyr Ser Leu Leu Leu  
1315 1320 1325

Ser Ser Tyr Pro Ile Ser Thr Asn Ile Asn Leu Ser Lys Asp Asp Leu  
1330 1335 1340

Trp Ile Phe Asn Ile Asp Asn Glu Val Arg Glu Ile Ser Ile Glu Asn  
1345 1350 1355 1360

Gly Thr Ile Lys Lys Gly Lys Leu Ile Lys Asp Val Leu Ser Lys Ile  
1365 1370 1375

Asp Ile Asn Lys Asn Lys Leu Ile Ile Gly Asn Gln Thr Ile Asp Phe  
1380 1385 1390

Ser Gly Asp Ile Asp Asn Lys Asp Arg Tyr Ile Phe Leu Thr Cys Glu  
1395 1400 1405

Leu Asp Asp Lys Ile Ser Leu Ile Ile Glu Ile Asn Leu Val Ala Lys  
1410 1415 1420

Ser Tyr Ser Leu Leu Ser Gly Asp Lys Asn Tyr Leu Ile Ser Asn  
1425 1430 1435 1440

Leu Ser Asn Thr Ile Glu Lys Ile Asn Thr Leu Gly Leu Asp Ser Lys  
1445 1450 1455

Asn Ile Ala Tyr Asn Tyr Thr Asp Glu Ser Asn Asn Lys Tyr Phe Gly  
1460 1465 1470

Ala Ile Ser Lys Thr Ser Gln Lys Ser Ile Ile His Tyr Lys Lys Asp  
1475 1480 1485

Ser Lys Asn Ile Leu Glu Phe Tyr Asn Asp Ser Thr Leu Glu Phe Asn  
1490 1495 1500

Ser Lys Asp Phe Ile Ala Glu Asp Ile Asn Val Phe Met Lys Asp Asp  
1505 1510 1515 1520

Ile Asn Thr Ile Thr Gly Lys Tyr Tyr Val Asp Asn Asn Thr Asp Lys  
1525 1530 1535

Ser Ile Asp Phe Ser Ile Ser Leu Val Ser Lys Asn Gln Val Lys Val  
 1540 1545 1550  
 Asn Gly Leu Tyr Leu Asn Glu Ser Val Tyr Ser Ser Tyr Leu Asp Phe  
 1555 1560 1565  
 Val Lys Asn Ser Asp Gly His His Asn Thr Ser Asn Phe Met Asn Leu  
 1570 1575 1580  
 Phe Leu Asp Asn Ile Ser Phe Trp Lys Leu Phe Gly Phe Glu Asn Ile  
 1585 1590 1595 1600  
 Asn Phe Val Ile Asp Lys Tyr Phe Thr Leu Val Gly Lys Thr Asn Leu  
 1605 1610 1615  
 Gly Tyr Val Glu Phe Ile Cys Asp Asn Asn Lys Asn Ile Asp Ile Tyr  
 1620 1625 1630  
 Phe Gly Glu Trp Lys Thr Ser Ser Lys Ser Thr Ile Phe Ser Gly  
 1635 1640 1645  
 Asn Gly Arg Asn Val Val Val Glu Pro Ile Tyr Asn Pro Asp Thr Gly  
 1650 1655 1660  
 Glu Asp Ile Ser Thr Ser Leu Asp Phe Ser Tyr Glu Pro Leu Tyr Gly  
 1665 1670 1675 1680  
 Ile Asp Arg Tyr Ile Asn Lys Val Leu Ile Ala Pro Asp Leu Tyr Thr  
 1685 1690 1695  
 Ser Leu Ile Asn Ile Asn Thr Asn Tyr Tyr Ser Asn Glu Tyr Tyr Pro  
 1700 1705 1710  
 Glu Ile Ile Val Leu Asn Pro Asn Thr Phe His Lys Lys Val Asn Ile  
 1715 1720 1725  
 Asn Leu Asp Ser Ser Ser Phe Glu Tyr Lys Trp Ser Thr Glu Gly Ser  
 1730 1735 1740  
 Asp Phe Ile Leu Val Arg Tyr Leu Glu Glu Ser Asn Lys Lys Ile Leu  
 1745 1750 1755 1760  
 Gln Lys Ile Arg Ile Lys Gly Ile Leu Ser Asn Thr Gln Ser Phe Asn  
 1765 1770 1775  
 Lys Met Ser Ile Asp Phe Lys Asp Ile Lys Lys Leu Ser Leu Gly Tyr  
 1780 1785 1790  
 Ile Met Ser Asn Phe Lys Ser Phe Asn Ser Glu Asn Glu Leu Asp Arg  
 1795 1800 1805  
 Asp His Leu Gly Phe Lys Ile Ile Asp Asn Lys Thr Tyr Tyr Tyr Asp  
 1810 1815 1820  
 Glu Asp Ser Lys Leu Val Lys Gly Leu Ile Asn Ile Asn Asn Ser Leu  
 1825 1830 1835 1840  
 Phe Tyr Phe Asp Pro Ile Glu Phe Asn Leu Val Thr Gly Trp Gln Thr  
 1845 1850 1855  
 Ile Asn Gly Lys Lys Tyr Tyr Phe Asp Ile Asn Thr Gly Ala Ala Leu  
 1860 1865 1870

Thr Ser Tyr Lys Ile Ile Asn Gly Lys His Phe Tyr Phe Asn Asn Asp  
1875 1880 1885

Gly Val Met Gln Leu Gly Val Phe Lys Gly Pro Asp Gly Phe Glu Tyr  
1890 1895 1900

Phe Ala Pro Ala Asn Thr Gln Asn Asn Asn Ile Glu Gly Gln Ala Ile  
1905 1910 1915 1920

Val Tyr Gln Ser Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe  
1925 1930 1935

Asp Asn Asn Ser Lys Ala Val Thr Gly Trp Arg Ile Ile Asn Asn Glu  
1940 1945 1950

Lys Tyr Tyr Phe Asn Pro Asn Asn Ala Ile Ala Ala Val Gly Leu Gln  
1955 1960 1965

Val Ile Asp Asn Asn Lys Tyr Tyr Phe Asn Pro Asp Thr Ala Ile Ile  
1970 1975 1980

Ser Lys Gly Trp Gln Thr Val Asn Gly Ser Arg Tyr Tyr Phe Asp Thr  
1985 1990 1995 2000

Asp Thr Ala Ile Ala Phe Asn Gly Tyr Lys Thr Ile Asp Gly Lys His  
2005 2010 2015

Phe Tyr Phe Asp Ser Asp Cys Val Val Lys Ile Gly Val Phe Ser Thr  
2020 2025 2030

Ser Asn Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Tyr Asn Asn Asn  
2035 2040 2045

Ile Glu Gly Gln Ala Ile Val Tyr Gln Ser Lys Phe Leu Thr Leu Asn  
2050 2055 2060

Gly Lys Lys Tyr Tyr Phe Asp Asn Asn Ser Lys Ala Val Thr Gly Leu  
2065 2070 2075 2080

Gln Thr Ile Asp Ser Lys Lys Tyr Tyr Phe Asn Thr Asn Thr Ala Glu  
2085 2090 2095

Ala Ala Thr Gly Trp Gln Thr Ile Asp Gly Lys Tyr Tyr Phe Asn  
2100 2105 2110

Thr Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile Asp Gly Lys  
2115 2120 2125

Lys Tyr Tyr Phe Asn Thr Asn Thr Ala Ile Ala Ser Thr Gly Tyr Thr  
2130 2135 2140

Ile Ile Asn Gly Lys His Phe Tyr Phe Asn Thr Asp Gly Ile Met Gln  
2145 2150 2155 2160

Ile Gly Val Phe Lys Gly Pro Asn Gly Phe Glu Tyr Phe Ala Pro Ala  
2165 2170 2175

Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile Leu Tyr Gln Asn  
2180 2185 2190

Glu Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Gly Ser Asp Ser  
2195 2200 2205

Lys Ala Val Thr Gly Trp Arg Ile Ile Asn Asn Lys Lys Tyr Tyr Phe  
2210 2215 2220

Asn Pro Asn Asn Ala Ile Ala Ala Ile His Leu Cys Thr Ile Asn Asn  
2225 2230 2235 2240

Asp Lys Tyr Tyr Phe Ser Tyr Asp Gly Ile Leu Gln Asn Gly Tyr Ile  
2245 2250 2255

Thr Ile Glu Arg Asn Asn Phe Tyr Phe Asp Ala Asn Asn Glu Ser Lys  
2260 2265 2270

Met Val Thr Gly Val Phe Lys Gly Pro Asn Gly Phe Glu Tyr Phe Ala  
2275 2280 2285

Pro Ala Asn Thr His Asn Asn Ile Glu Gly Gln Ala Ile Val Tyr  
2290 2295 2300

Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Asp Asn  
2305 2310 2315 2320

Asp Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr  
2325 2330 2335

Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile  
2340 2345 2350

Asp Gly Lys Lys Tyr Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr  
2355 2360 2365

Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr  
2370 2375 2380

Phe Ile Ala Ser Thr Gly Tyr Thr Ser Ile Asn Gly Lys His Phe Tyr  
2385 2390 2395 2400

Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro Asn  
2405 2410 2415

Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu  
2420 2425 2430

Gly Gln Ala Ile Leu Tyr Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys  
2435 2440 2445

Lys Tyr Tyr Phe Gly Ser Asp Ser Lys Ala Val Thr Gly Leu Arg Thr  
2450 2455 2460

Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr Ala Val Ala Val  
2465 2470 2475 2480

Thr Gly Trp Gln Thr Ile Asn Gly Lys Lys Tyr Tyr Phe Asn Thr Asn  
2485 2490 2495

Thr Ser Ile Ala Ser Thr Gly Tyr Thr Ile Ile Ser Gly Lys His Phe  
2500 2505 2510

Tyr Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro  
2515 2520 2525

Asp Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile  
2530 2535 2540

Glu Gly Gln Ala Ile Arg Tyr Gln Asn Arg Phe Leu Tyr Leu His Asp  
 2545 2550 2555 2560  
 Asn Ile Tyr Tyr Phe Gly Asn Asn Ser Lys Ala Ala Thr Gly Trp Val  
 2565 2570 2575  
 Thr Ile Asp Gly Asn Arg Tyr Tyr Phe Glu Pro Asn Thr Ala Met Gly  
 2580 2585 2590  
 Ala Asn Gly Tyr Lys Thr Ile Asp Asn Lys Asn Phe Tyr Phe Arg Asn  
 2595 2600 2605  
 Gly Leu Pro Gln Ile Gly Val Phe Lys Gly Ser Asn Gly Phe Glu Tyr  
 2610 2615 2620  
 Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile  
 2625 2630 2635 2640  
 Arg Tyr Gln Asn Arg Phe Leu His Leu Leu Gly Lys Ile Tyr Tyr Phe  
 2645 2650 2655  
 Gly Asn Asn Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asn Gly Lys  
 2660 2665 2670  
 Val Tyr Tyr Phe Met Pro Asp Thr Ala Met Ala Ala Ala Gly Gly Leu  
 2675 2680 2685  
 Phe Glu Ile Asp Gly Val Ile Tyr Phe Phe Gly Val Asp Gly Val Lys  
 2690 2695 2700  
 Ala Pro Gly Ile Tyr Gly  
 2705 2710

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 811 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Tyr Lys Ile Ile Asn Gly Lys His Phe Tyr Phe Asn Asn Asp Gly  
 1 5 10 15  
 Val Met Gln Leu Gly Val Phe Lys Gly Pro Asp Gly Phe Glu Tyr Phe  
 20 25 30  
 Ala Pro Ala Asn Thr Gln Asn Asn Asn Ile Glu Gly Gln Ala Ile Val  
 35 40 45  
 Tyr Gln Ser Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Asp  
 50 55 60  
 Asn Asn Ser Lys Ala Val Thr Gly Trp Arg Ile Ile Asn Asn Glu Lys  
 65 70 75 80  
 Tyr Tyr Phe Asn Pro Asn Asn Ala Ile Ala Ala Val Gly Leu Gln Val  
 85 90 95

Ile Asp Asn Asn Lys Tyr Tyr Phe Asn Pro Asp Thr Ala Ile Ile Ser  
 100 105 110  
 Lys Gly Trp Gln Thr Val Asn Gly Ser Arg Tyr Tyr Phe Asp Thr Asp  
 115 120 125  
 Thr Ala Ile Ala Phe Asn Gly Tyr Lys Thr Ile Asp Gly Lys His Phe  
 130 135 140  
 Tyr Phe Asp Ser Asp Cys Val Val Lys Ile Gly Val Phe Ser Thr Ser  
 145 150 155 160  
 Asn Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Tyr Asn Asn Asn Ile  
 165 170 175  
 Glu Gly Gln Ala Ile Val Tyr Gln Ser Lys Phe Leu Thr Leu Asn Gly  
 180 185 190  
 Lys Lys Tyr Tyr Phe Asp Asn Asn Ser Lys Ala Val Thr Gly Leu Gln  
 195 200 205  
 Thr Ile Asp Ser Lys Lys Tyr Tyr Phe Asn Thr Asn Thr Ala Glu Ala  
 210 215 220  
 Ala Thr Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr  
 225 230 235 240  
 Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile Asp Gly Lys Lys  
 245 250 255  
 Tyr Tyr Phe Asn Thr Asn Thr Ala Ile Ala Ser Thr Gly Tyr Thr Ile  
 260 265 270  
 Ile Asn Gly Lys His Phe Tyr Phe Asn Thr Asp Gly Ile Met Gln Ile  
 275 280 285  
 Gly Val Phe Lys Gly Pro Asn Gly Phe Glu Tyr Phe Ala Pro Ala Asn  
 290 295 300  
 Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile Leu Tyr Gln Asn Glu  
 305 310 315 320  
 Phe Leu Thr Leu Asn Gly Lys Tyr Tyr Phe Gly Ser Asp Ser Lys  
 325 330 335  
 Ala Val Thr Gly Trp Arg Ile Ile Asn Asn Lys Lys Tyr Tyr Phe Asn  
 340 345 350  
 Pro Asn Asn Ala Ile Ala Ala Ile His Leu Cys Thr Ile Asn Asn Asp  
 355 360 365  
 Lys Tyr Tyr Phe Ser Tyr Asp Gly Ile Leu Gln Asn Gly Tyr Ile Thr  
 370 375 380  
 Ile Glu Arg Asn Asn Phe Tyr Phe Asp Ala Asn Asn Glu Ser Lys Met  
 385 390 395 400  
 Val Thr Gly Val Phe Lys Gly Pro Asn Gly Phe Glu Tyr Phe Ala Pro  
 405 410 415  
 Ala Asn Thr His Asn Asn Ile Glu Gly Gln Ala Ile Val Tyr Gln  
 420 425 430

Asn Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Asp Asn Asp  
 435 440 445  
 Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr  
 450 455 460  
 Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile Asp  
 465 470 475 480  
 Gly Lys Lys Tyr Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr Gly  
 485 490 495  
 Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr Phe  
 500 505 510  
 Ile Ala Ser Thr Gly Tyr Thr Ser Ile Asn Gly Lys His Phe Tyr Phe  
 515 520 525  
 Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro Asn Gly  
 530 535 540  
 Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly  
 545 550 555 560  
 Gln Ala Ile Leu Tyr Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys Lys  
 565 570 575  
 Tyr Tyr Phe Gly Ser Asp Ser Lys Ala Val Thr Gly Leu Arg Thr Ile  
 580 585 590  
 Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr Ala Val Ala Val Thr  
 595 600 605  
 Gly Trp Gln Thr Ile Asn Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr  
 610 615 620  
 Ser Ile Ala Ser Thr Gly Tyr Thr Ile Ile Ser Gly Lys His Phe Tyr  
 625 630 635 640  
 Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro Asp  
 645 650 655  
 Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu  
 660 665 670  
 Gly Gln Ala Ile Arg Tyr Gln Asn Arg Phe Leu Tyr Leu His Asp Asn  
 675 680 685  
 Ile Tyr Tyr Phe Gly Asn Asn Ser Lys Ala Ala Thr Gly Trp Val Thr  
 690 695 700  
 Ile Asp Gly Asn Arg Tyr Tyr Phe Glu Pro Asn Thr Ala Met Gly Ala  
 705 710 715 720  
 Asn Gly Tyr Lys Thr Ile Asp Asn Lys Asn Phe Tyr Phe Arg Asn Gly  
 725 730 735  
 Leu Pro Gln Ile Gly Val Phe Lys Gly Ser Asn Gly Phe Glu Tyr Phe  
 740 745 750  
 Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile Arg  
 755 760 765

Tyr Gln Asn Arg Phe Leu His Leu Leu Gly Lys Ile Tyr Tyr Phe Gly  
770 775 780

Asn Asn Ser Lys Ala Val Thr Gly Trp Gln Thr Ile Asn Gly Lys Val  
785 790 795 800

Tyr Tyr Phe Met Pro Asp Thr Ala Met Ala Ala  
805 810

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 91 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Tyr Lys Ile Ile Asn Gly Lys His Phe Tyr Phe Asn Asn Asp Gly  
1 5 10 15

Val Met Gln Leu Gly Val Phe Lys Gly Pro Asp Gly Phe Glu Tyr Phe  
20 25 30

Ala Pro Ala Asn Thr Gln Asn Asn Asn Ile Glu Gly Gln Ala Ile Val  
35 40 45

Tyr Gln Ser Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Asp  
50 55 60

Asn Asn Ser Lys Ala Val Thr Gly Trp Arg Ile Ile Asn Asn Glu Lys  
65 70 75 80

Tyr Tyr Phe Asn Pro Asn Asn Ala Ile Ala Ala  
85 90

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..7098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG AGT TTA GTT AAT AGA AAA CAG TTA GAA AAA ATG GCA AAT GTA AGA  
Met Ser Leu Val Asn Arg Lys Gln Leu Glu Lys Met Ala Asn Val Arg  
1 5 10 15 48

TTT CGT ACT CAA GAA GAT GAA TAT GTT GCA ATA TTG GAT GCT TTA GAA  
Phe Arg Thr Gln Glu Asp Glu Tyr Val Ala Ile Leu Asp Ala Leu Glu  
20 25 30 96

GAA TAT CAT AAT ATG TCA GAG AAT ACT GTA GTC GAA AAA TAT TTA AAA Glu Tyr His Asn Met Ser Glu Asn Thr Val Val Glu Lys Tyr Leu Lys 35 40 45	144
TTA AAA GAT ATA AAT AGT TTA ACA GAT ATT TAT ATA GAT ACA TAT AAA Leu Lys Asp Ile Asn Ser Leu Thr Asp Ile Tyr Ile Asp Thr Tyr Lys 50 55 60	192
AAA TCT GGT AGA AAT AAA GCC TTA AAA AAA TTT AAG GAA TAT CTA GTT Lys Ser Gly Arg Asn Lys Ala Leu Lys Lys Phe Lys Glu Tyr Leu Val 65 70 75 80	240
ACA GAA GTA TTA GAG CTA AAG AAT AAT TTA ACT CCA GTT GAG AAA Thr Glu Val Leu Glu Leu Lys Asn Asn Asn Leu Thr Pro Val Glu Lys 85 90 95	288
AAT TTA CAT TTT GTT TGG ATT GGA GGT CAA ATA AAT GAC ACT GCT ATT Asn Leu His Phe Val Trp Ile Gly Gly Gln Ile Asn Asp Thr Ala Ile 100 105 110	336
AAT TAT ATA AAT CAA TGG AAA GAT GTA AAT AGT GAT TAT AAT GTT AAT Asn Tyr Ile Asn Gln Trp Lys Asp Val Asn Ser Asp Tyr Asn Val Asn 115 120 125	384
GTT TTT TAT GAT AGT AAT GCA TTT TTG ATA AAC ACA TTG AAA AAA ACT Val Phe Tyr Asp Ser Asn Ala Phe Leu Ile Asn Thr Leu Lys Lys Thr 130 135 140	432
GTA GTA GAA TCA GCA ATA AAT GAT ACA CTT GAA TCA TTT AGA GAA AAC Val Val Glu Ser Ala Ile Asn Asp Thr Leu Glu Ser Phe Arg Glu Asn 145 150 155 160	480
TTA AAT GAC CCT AGA TTT GAC TAT AAT AAA TTC TTC AGA AAA CGT ATG Leu Asn Asp Pro Arg Phe Asp Tyr Asn Lys Phe Phe Arg Lys Arg Met 165 170 175	528
GAA ATA ATT TAT GAT AAA CAG AAA AAT TTC ATA AAC TAC TAT AAA GCT Glu Ile Ile Tyr Asp Lys Gln Lys Asn Phe Ile Asn Tyr Tyr Lys Ala 180 185 190	576
CAA AGA GAA GAA AAT CCT GAA CTT ATA ATT GAT GAT ATT GTA AAG ACA Gln Arg Glu Glu Asn Pro Glu Leu Ile Ile Asp Asp Ile Val Lys Thr 195 200 205	624
TAT CTT TCA AAT GAG TAT TCA AAG GAG ATA GAT GAA CTT AAT ACC TAT Tyr Leu Ser Asn Glu Tyr Ser Lys Glu Ile Asp Glu Leu Asn Thr Tyr 210 215 220	672
ATT GAA GAA TCC TTA AAT AAA ATT ACA CAG AAT AGT GGA AAT GAT GTT Ile Glu Glu Ser Leu Asn Lys Ile Thr Gln Asn Ser Gly Asn Asp Val 225 230 235 240	720
AGA AAC TTT GAA GAA TTT AAA AAT GGA GAG TCA TTC AAC TTA TAT GAA Arg Asn Phe Glu Glu Phe Lys Asn Gly Glu Ser Phe Asn Leu Tyr Glu 245 250 255	768
CAA GAG TTG GTA GAA AGG TGG AAT TTA GCT GCT GCT TCT GAC ATA TTA Gln Glu Leu Val Glu Arg Trp Asn Leu Ala Ala Ser Asp Ile Leu 260 265 270	816
AGA ATA TCT GCA TTA AAA GAA ATT GGT GGT ATG TAT TTA GAT GTT GAT Arg Ile Ser Ala Leu Lys Glu Ile Gly Gly Met Tyr Leu Asp Val Asp	864

275	280	285	
ATG TTA CCA GGA ATA CAA CCA GAC TTA TTT GAG TCT ATA GAG AAA CCT Met Leu Pro Gly Ile Gln Pro Asp Leu Phe Glu Ser Ile Glu Lys Pro 290 295 300			912
AGT TCA GTA ACA GTG GAT TTT TGG GAA ATG ACA AAG TTA GAA GCT ATA Ser Ser Val Thr Val Asp Phe Trp Glu Met Thr Lys Leu Glu Ala Ile 305 310 315 320			960
ATG AAA TAC AAA GAA TAT ATA CCA GAA TAT ACC TCA GAA CAT TTT GAC Met Lys Tyr Lys Glu Tyr Ile Pro Glu Tyr Thr Ser Glu His Phe Asp 325 330 335			1008
ATG TTA GAC GAA GAA GTT CAA AGT AGT TTT GAA TCT GTT CTA GCT TCT Met Leu Asp Glu Glu Val Gln Ser Ser Phe Glu Ser Val Leu Ala Ser 340 345 350			1056
AAG TCA GAT AAA TCA GAA ATA TTC TCA TCA CTT GGT GAT ATG GAG GCA Lys Ser Asp Lys Ser Glu Ile Phe Ser Ser Leu Gly Asp Met Glu Ala 355 360 365			1104
TCA CCA CTA GAA GTT AAA ATT GCA TTT AAT AGT AAG GGT ATT ATA AAT Ser Pro Leu Glu Val Lys Ile Ala Phe Asn Ser Lys Gly Ile Ile Asn 370 375 380			1152
CAA GGG CTA ATT TCT GTG AAA GAC TCA TAT TGT AGC AAT TTA ATA GTA Gln Gly Leu Ile Ser Val Lys Asp Ser Tyr Cys Ser Asn Leu Ile Val 385 390 395 400			1200
AAA CAA ATC GAG AAT AGA TAT AAA ATA TTG AAT AAT AGT TTA AAT CCA Lys Gln Ile Glu Asn Arg Tyr Lys Ile Leu Asn Asn Ser Leu Asn Pro 405 410 415			1248
GCT ATT AGC GAG GAT AAT GAT TTT AAT ACT ACA ACG AAT ACC TTT ATT Ala Ile Ser Glu Asp Asn Asp Phe Asn Thr Thr Asn Thr Phe Ile 420 425 430			1296
GAT AGT ATA ATG GCT GAA GCT AAT GCA GAT AAT GGT AGA TTT ATG ATG Asp Ser Ile Met Ala Glu Ala Asn Ala Asp Asn Gly Arg Phe Met Met 435 440 445			1344
GAA CTA GGA AAG TAT TTA AGA GTT GGT TTC TTC CCA GAT GTT AAA ACT Glu Leu Gly Lys Tyr Leu Arg Val Gly Phe Phe Pro Asp Val Lys Thr 450 455 460			1392
ACT ATT AAC TTA AGT GGC CCT GAA GCA TAT GCG GCA GCT TAT CAA GAT Thr Ile Asn Leu Ser Gly Pro Glu Ala Tyr Ala Ala Tyr Gln Asp 465 470 475 480			1440
TTA TTA ATG TTT AAA GAA GGC AGT ATG AAT ATC CAT TTG ATA GAA GCT Leu Leu Met Phe Lys Glu Gly Ser Met Asn Ile His Leu Ile Glu Ala 485 490 495			1488
GAT TTA AGA AAC TTT GAA ATC TCT AAA ACT AAT ATT TCT CAA TCA ACT Asp Leu Arg Asn Phe Glu Ile Ser Lys Thr Asn Ile Ser Gln Ser Thr 500 505 510			1536
GAA CAA GAA ATG GCT AGC TTA TGG TCA TTT GAC GAT GCA AGA GCT AAA Glu Gln Glu Met Ala Ser Leu Trp Ser Phe Asp Asp Ala Arg Ala Lys 515 520 525			1584

GCT CAA TTT GAA GAA TAT AAA AGG AAT TAT TTT GAA GGT TCT CTT GGT Ala Gln Phe Glu Glu Tyr Lys Arg Asn Tyr Phe Glu Gly Ser Leu Gly 530 535 540	1632
GAA GAT GAT AAT CTT GAT TTT TCT CAA AAT ATA GTA GTT GAC AAG GAG Glu Asp Asp Asn Leu Asp Phe Ser Gln Asn Ile Val Val Asp Lys Glu 545 550 555 560	1680
TAT CTT TTA GAA AAA ATA TCT TCA TTA GCA AGA AGT TCA GAG AGA GGA Tyr Leu Leu Glu Lys Ile Ser Ser Leu Ala Arg Ser Ser Glu Arg Gly 565 570 575	1728
TAT ATA CAC TAT ATT GTT CAG TTA CAA GGA GAT AAA ATT AGT TAT GAA Tyr Ile His Tyr Ile Val Gln Leu Gln Gly Asp Lys Ile Ser Tyr Glu 580 585 590	1776
GCA GCA TGT AAC TTA TTT GCA AAG ACT CCT TAT GAT AGT GTA CTG TTT Ala Ala Cys Asn Leu Phe Ala Lys Thr Pro Tyr Asp Ser Val Leu Phe 595 600 605	1824
CAG AAA AAT ATA GAA GAT TCA GAA ATT GCA TAT TAT TAT AAT CCT GGA Gln Lys Asn Ile Glu Asp Ser Glu Ile Ala Tyr Tyr Tyr Asn Pro Gly 610 615 620	1872
GAT GGT GAA ATA CAA GAA ATA GAC AAG TAT AAA ATT CCA AGT ATA ATT Asp Gly Glu Ile Gln Glu Ile Asp Lys Tyr Lys Ile Pro Ser Ile Ile 625 630 635 640	1920
TCT GAT AGA CCT AAG ATT AAA TTA ACA TTT ATT GGT CAT GGT AAA GAT Ser Asp Arg Pro Lys Ile Lys Leu Thr Phe Ile Gly His Gly Lys Asp 645 650 655	1968
GAA TTT AAT ACT GAT ATA TTT GCA GGT TTT GAT GTA GAT TCA TTA TCC Glu Phe Asn Thr Asp Ile Phe Ala Gly Phe Asp Val Asp Ser Leu Ser 660 665 670	2016
ACA GAA ATA GAA GCA GCA ATA GAT TTA GCT AAA GAG GAT ATT TCT CCT Thr Glu Ile Glu Ala Ala Ile Asp Leu Ala Lys Glu Asp Ile Ser Pro 675 680 685	2064
AAG TCA ATA GAA ATA AAT TTA TTA GGA TGT AAT ATG TTT AGC TAC TCT Lys Ser Ile Glu Ile Asn Leu Leu Gly Cys Asn Met Phe Ser Tyr Ser 690 695 700	2112
ATC AAC GTA GAG GAG ACT TAT CCT GGA AAA TTA TTA CTT AAA GTT AAA Ile Asn Val Glu Glu Thr Tyr Pro Gly Lys Leu Leu Leu Lys Val Lys 705 710 715 720	2160
GAT AAA ATA TCA GAA TTA ATG CCA TCT ATA AGT CAA GAC TCT ATT ATA Asp Lys Ile Ser Glu Leu Met Pro Ser Ile Ser Gln Asp Ser Ile Ile 725 730 735	2208
GTA AGT GCA AAT CAA TAT GAA GTT AGA ATA AAT AGT GAA GGA AGA AGA Val Ser Ala Asn Gln Tyr Glu Val Arg Ile Asn Ser Glu Gly Arg Arg 740 745 750	2256
GAA TTA TTG GAT CAT TCT GGT GAA TGG ATA AAT AAA GAA GAA AGT ATT Glu Leu Leu Asp His Ser Gly Glu Trp Ile Asn Lys Glu Glu Ser Ile 755 760 765	2304

ATA AAG GAT ATT TCA TCA AAA GAA TAT ATA TCA TTT AAT CCT AAA GAA Ile Lys Asp Ile Ser Ser Lys Glu Tyr Ile Ser Phe Asn Pro Lys Glu 770 775 780	2352
AAT AAA ATT ACA GTA AAA TCT AAA AAT TTA CCT GAG CTA TCT ACA TTA Asn Lys Ile Thr Val Lys Ser Lys Asn Leu Pro Glu Leu Ser Thr Leu 785 790 795 800	2400
TTA CAA GAA ATT AGA AAT AAT TCT AAT TCA AGT GAT ATT GAA CTA GAA Leu Gln Glu Ile Arg Asn Asn Ser Ser Asp Ile Glu Leu Glu 805 810 815	2448
GAA AAA GTA ATG TTA ACA GAA TGT GAG ATA AAT GTT ATT TCA AAT ATA Glu Lys Val Met Leu Thr Glu Cys Glu Ile Asn Val Ile Ser Asn Ile 820 825 830	2496
GAT ACG CAA ATT GTT GAG GAA AGG ATT GAA GAA GCT AAG AAT TTA ACT Asp Thr Gln Ile Val Glu Glu Arg Ile Glu Glu Ala Lys Asn Leu Thr 835 840 845	2544
TCT GAC TCT ATT AAT TAT ATA AAA GAT GAA TTT AAA CTA ATA GAA TCT Ser Asp Ser Ile Asn Tyr Ile Lys Asp Glu Phe Lys Leu Ile Glu Ser 850 855 860	2592
ATT TCT GAT GCA CTA TGT GAC TTA AAA CAA CAG AAT GAA TTA GAA GAT Ile Ser Asp Ala Leu Cys Asp Leu Lys Gln Gln Asn Glu Leu Glu Asp 865 870 875 880	2640
TCT CAT TTT ATA TCT TTT GAG GAC ATA TCA GAG ACT GAT GAG GGA TTT Ser His Phe Ile Ser Phe Glu Asp Ile Ser Glu Thr Asp Glu Gly Phe 885 890 895	2688
AGT ATA AGA TTT ATT AAT AAA GAA ACT GGA GAA TCT ATA TTT GTA GAA Ser Ile Arg Phe Ile Asn Lys Glu Thr Gly Glu Ser Ile Phe Val Glu 900 905 910	2736
ACT GAA AAA ACA ATA TTC TCT GAA TAT GCT AAT CAT ATA ACT GAA GAG Thr Glu Lys Thr Ile Phe Ser Glu Tyr Ala Asn His Ile Thr Glu Glu 915 920 925	2784
ATT TCT AAG ATA AAA GGT ACT ATA TTT GAT ACT GTA AAT GGT AAG TTA Ile Ser Lys Ile Lys Gly Thr Ile Phe Asp Thr Val Asn Gly Lys Leu 930 935 940	2832
GTA AAA AAA GTA AAT TTA GAT ACT ACA CAC GAA GTA AAT ACT TTA AAT Val Lys Lys Val Asn Leu Asp Thr Thr His Glu Val Asn Thr Leu Asn 945 950 955 960	2880
GCT GCA TTT ATA CAA TCA TTA ATA GAA TAT AAT AGT TCT AAA GAA Ala Ala Phe Phe Ile Gln Ser Leu Ile Glu Tyr Asn Ser Ser Lys Glu 965 970 975	2928
TCT CTT AGT AAT TTA AGT GTA GCA ATG AAA GTC CAA GTT TAC GCT CAA Ser Leu Ser Asn Leu Ser Val Ala Met Lys Val Gln Val Tyr Ala Gln 980 985 990	2976
TTA TTT AGT ACT GGT TTA AAT ACT ATT ACA GAT GCA GCC AAA GTT GTT Leu Phe Ser Thr Gly Leu Asn Thr Ile Thr Asp Ala Ala Lys Val Val 995 1000 1005	3024

GAA TTA GTA TCA ACT GCA TTA GAT GAA ACT ATA GAC TTA CTT CCT ACA Glu Leu Val Ser Thr Ala Leu Asp Glu Thr Ile Asp Leu Leu Pro Thr 1010 1015 1020	3072
TTA TCT GAA GGA TTA CCT ATA ATT GCA ACT ATT ATA GAT GGT GTA AGT Leu Ser Glu Gly Leu Pro Ile Ile Ala Thr Ile Ile Asp Gly Val Ser 1025 1030 1035 1040	3120
TTA GGT GCA GCA ATC AAA GAG CTA AGT GAA ACG AGT GAC CCA TTA TTA Leu Gly Ala Ala Ile Lys Glu Leu Ser Glu Thr Ser Asp Pro Leu Leu 1045 1050 1055	3168
AGA CAA GAA ATA GAA GCT AAG ATA GGT ATA ATG GCA GTA AAT TTA ACA Arg Gln Glu Ile Glu Ala Lys Ile Gly Ile Met Ala Val Asn Leu Thr 1060 1065 1070	3216
ACA GCT ACA ACT GCA ATC ATT ACT TCA TCT TTG GGG ATA GCT AGT GGA Thr Ala Thr Ala Ile Ile Thr Ser Ser Leu Gly Ile Ala Ser Gly 1075 1080 1085	3264
TTT AGT ATA CTT TTA GTT CCT TTA GCA GGA ATT TCA GCA GGT ATA CCA Phe Ser Ile Leu Leu Val Pro Leu Ala Gly Ile Ser Ala Gly Ile Pro 1090 1095 1100	3312
AGC TTA GTA AAC AAT GAA CTT GTA CTT CGA GAT AAG GCA ACA AAG GTT Ser Leu Val Asn Asn Glu Leu Val Leu Arg Asp Lys Ala Thr Lys Val 1105 1110 1115 1120	3360
GTA GAT TAT TTT AAA CAT GTT TCA TTA GTT GAA ACT GAA GGA GTA TTT Val Asp Tyr Phe Lys His Val Ser Leu Val Glu Thr Glu Gly Val Phe 1125 1130 1135	3408
ACT TTA TTA GAT GAT AAA ATA ATG ATG CCA CAA GAT GAT TTA GTG ATA Thr Leu Leu Asp Asp Lys Ile Met Met Pro Gln Asp Asp Leu Val Ile 1140 1145 1150	3456
TCA GAA ATA GAT TTT AAT AAT TCA ATA GTT TTA GGT AAA TGT GAA Ser Glu Ile Asp Phe Asn Asn Ser Ile Val Leu Gly Lys Cys Glu 1155 1160 1165	3504
ATC TGG AGA ATG GAA GGT GGT TCA GGT CAT ACT GTA ACT GAT GAT ATA Ile Trp Arg Met Glu Gly Gly Ser Gly His Thr Val Thr Asp Asp Ile 1170 1175 1180	3552
GAT CAC TTC TTT TCA GCA CCA TCA ATA ACA TAT AGA GAG CCA CAC TTA Asp His Phe Phe Ser Ala Pro Ser Ile Thr Tyr Arg Glu Pro His Leu 1185 1190 1195 1200	3600
TCT ATA TAT GAC GTA TTG GAA GTA CAA AAA GAA GAA CTT GAT TTG TCA Ser Ile Tyr Asp Val Leu Glu Val Gln Lys Glu Glu Leu Asp Leu Ser 1205 1210 1215	3648
AAA GAT TTA ATG GTA TTA CCT AAT GCT CCA AAT AGA GTA TTT GCT TGG Lys Asp Leu Met Val Leu Pro Asn Ala Pro Asn Arg Val Phe Ala Trp 1220 1225 1230	3696
GAA ACA GGA TGG ACA CCA GGT TTA AGA AGC TTA GAA AAT GAT GGC ACA Glu Thr Gly Trp Thr Pro Gly Leu Arg Ser Leu Glu Asn Asp Gly Thr 1235 1240 1245	3744

AAA CTG TTA GAC CGT ATA AGA GAT AAC TAT GAA GGT GAG TTT TAT TGG Lys Leu Leu Asp Arg Ile Arg Asp Asn Tyr Glu Gly Glu Phe Tyr Trp 1250 1255 1260	3792
AGA TAT TTT GCT TTT ATA GCT GAT GCT TTA ATA ACA ACA TTA AAA CCA Arg Tyr Phe Ala Phe Ile Ala Asp Ala Leu Ile Thr Thr Leu Lys Pro 1265 1270 1275 1280	3840
AGA TAT GAA GAT ACT AAT ATA AGA ATA AAT TTA GAT AGT AAT ACT AGA Arg Tyr Glu Asp Thr Asn Ile Arg Ile Asn Leu Asp Ser Asn Thr Arg 1285 1290 1295	3888
AGT TTT ATA GTT CCA ATA ATA ACT ACA GAA TAT ATA AGA GAA AAA TTA Ser Phe Ile Val Pro Ile Ile Thr Thr Glu Tyr Ile Arg Glu Lys Leu 1300 1305 1310	3936
TCA TAT TCT TTC TAT GGT TCA GGA GGA ACT TAT GCA TTG TCT CTT TCT Ser Tyr Ser Phe Tyr Gly Ser Gly Gly Thr Tyr Ala Leu Ser Leu Ser 1315 1320 1325	3984
CAA TAT AAT ATG GGT ATA AAT ATA GAA TTA AGT GAA AGT GAT GTT TGG Gln Tyr Asn Met Gly Ile Asn Ile Glu Leu Ser Glu Ser Asp Val Trp 1330 1335 1340	4032
ATT ATA GAT GTT GAT AAT GTT GTG AGA GAT GTA ACT ATA GAA TCT GAT Ile Ile Asp Val Asp Asn Val Val Arg Asp Val Thr Ile Glu Ser Asp 1345 1350 1355 1360	4080
AAA ATT AAA AAA GGT GAT TTA ATA GAA GGT ATT TTA TCT ACA CTA AGT Lys Ile Lys Lys Gly Asp Leu Ile Glu Gly Ile Leu Ser Thr Leu Ser 1365 1370 1375	4128
ATT GAA GAG AAT AAA ATT ATC TTA AAT AGC CAT GAG ATT AAT TTT TCT Ile Glu Glu Asn Lys Ile Ile Leu Asn Ser His Glu Ile Asn Phe Ser 1380 1385 1390	4176
GGT GAG GTA AAT GGA AGT AAT GGA TTT GTT TCT TTA ACA TTT TCA ATT Gly Glu Val Asn Gly Ser Asn Gly Phe Val Ser Leu Thr Phe Ser Ile 1395 1400 1405	4224
TTA GAA GGA ATA AAT GCA ATT ATA GAA GTT GAT TTA TTA TCT AAA TCA Leu Glu Gly Ile Asn Ala Ile Ile Glu Val Asp Leu Leu Ser Lys Ser 1410 1415 1420	4272
TAT AAA TTA CTT ATT TCT GGC GAA TTA AAA ATA TTG ATG TTA AAT TCA Tyr Lys Leu Leu Ile Ser Gly Glu Leu Lys Ile Leu Met Leu Asn Ser 1425 1430 1435 1440	4320
AAT CAT ATT CAA CAG AAA ATA GAT TAT ATA GGA TTC AAT AGC GAA TTA Asn His Ile Gln Gln Lys Ile Asp Tyr Ile Gly Phe Asn Ser Glu Leu 1445 1450 1455	4368
CAG AAA AAT ATA CCA TAT AGC TTT GTA GAT AGT GAA GGA AAA GAG AAT Gln Lys Asn Ile Pro Tyr Ser Phe Val Asp Ser Glu Gly Lys Glu Asn 1460 1465 1470	4416
GGT TTT ATT AAT GGT TCA ACA AAA GAA GGT TTA TTT GTA TCT GAA TTA Gly Phe Ile Asn Gly Ser Thr Lys Glu Gly Leu Phe Val Ser Glu Leu 1475 1480 1485	4464

CCT GAT GTA GTT CTT ATA AGT AAG GTT TAT ATG GAT GAT AGT AAG CCT Pro Asp Val Val Leu Ile Ser Lys Val Tyr Met Asp Asp Ser Lys Pro 1490 1495 1500	4512
TCA TTT GGA TAT TAT AGT AAT AAT TTG AAA GAT GTC AAA GTT ATA ACT Ser Phe Gly Tyr Tyr Ser Asn Asn Leu Lys Asp Val Lys Val Ile Thr 1505 1510 1515 1520	4560
AAA GAT AAT GTT AAT ATA TTA ACA GGT TAT TAT CTT AAG GAT GAT ATA Lys Asp Asn Val Asn Ile Leu Thr Gly Tyr Tyr Leu Lys Asp Asp Ile 1525 1530 1535	4608
AAA ATC TCT CTT TCT TTG ACT CTA CAA GAT GAA AAA ACT ATA AAG TTA Lys Ile Ser Leu Ser Leu Thr Leu Gln Asp Glu Lys Thr Ile Lys Leu 1540 1545 1550	4656
AAT AGT GTG CAT TTA GAT GAA AGT GGA GTA GCT GAG ATT TTG AAG TTC Asn Ser Val His Leu Asp Glu Ser Gly Val Ala Glu Ile Leu Lys Phe 1555 1560 1565	4704
ATG AAT AGA AAA GGT AAT ACA AAT ACT TCA GAT TCT TTA ATG AGC TTT Met Asn Arg Lys Gly Asn Thr Asn Thr Ser Asp Ser Leu Met Ser Phe 1570 1575 1580	4752
TTA GAA AGT ATG AAT ATA AAA AGT ATT TTC GTT AAT TTC TTA CAA TCT Leu Glu Ser Met Asn Ile Lys Ser Ile Phe Val Asn Phe Leu Gln Ser 1585 1590 1595 1600	4800
AAT ATT AAG TTT ATA TTA GAT GCT AAT TTT ATA ATA AGT GGT ACT ACT Asn Ile Lys Phe Ile Leu Asp Ala Asn Phe Ile Ile Ser Gly Thr Thr 1605 1610 1615	4848
TCT ATT GGC CAA TTT GAG TTT ATT TGT GAT GAA AAT GAT AAT ATA CAA Ser Ile Gly Gln Phe Glu Phe Ile Cys Asp Glu Asn Asp Asn Ile Gln 1620 1625 1630	4896
CCA TAT TTC ATT AAG TTT AAT ACA CTA GAA ACT AAT TAT ACT TTA TAT Pro Tyr Phe Ile Lys Phe Asn Thr Leu Glu Thr Asn Tyr Thr Leu Tyr 1635 1640 1645	4944
GTA GGA AAT AGA CAA AAT ATG ATA GTG GAA CCA AAT TAT GAT TTA GAT Val Gly Asn Arg Gln Asn Met Ile Val Glu Pro Asn Tyr Asp Leu Asp 1650 1655 1660	4992
GAT TCT GGA GAT ATA TCT TCA ACT GTT ATC AAT TTC TCT CAA AAG TAT Asp Ser Gly Asp Ile Ser Ser Thr Val Ile Asn Phe Ser Gln Lys Tyr 1665 1670 1675 1680	5040
CTT TAT GGA ATA GAC AGT TGT GTT AAT AAA GTT GTA ATT TCA CCA AAT Leu Tyr Gly Ile Asp Ser Cys Val Asn Lys Val Val Ile Ser Pro Asn 1685 1690 1695	5088
ATT TAT ACA GAT GAA ATA AAT ATA ACG CCT GTA TAT GAA ACA AAT AAT Ile Tyr Thr Asp Glu Ile Asn Ile Thr Pro Val Tyr Glu Thr Asn Asn 1700 1705 1710	5136
ACT TAT CCA GAA GTT ATT GTA TTA GAT GCA AAT TAT ATA AAT GAA AAA Thr Tyr Pro Glu Val Ile Val Leu Asp Ala Asn Tyr Ile Asn Glu Lys 1715 1720 1725	5184

ATA AAT GTT AAT ATC AAT GAT CTA TCT ATA CGA TAT GTA TGG AGT AAT Ile Asn Val Asn Ile Asn Asp Leu Ser Ile Arg Tyr Val Trp Ser Asn 1730 1735 1740	5232
GAT GGT AAT GAT TTT ATT CTT ATG TCA ACT AGT GAA GAA AAT AAG GTG Asp Gly Asn Asp Phe Ile Leu Met Ser Thr Ser Glu Glu Asn Lys Val 1745 1750 1755 1760	5280
TCA CAA GTT AAA ATA AGA TTC GTT AAT GTT TTT AAA GAT AAG ACT TTG Ser Gln Val Lys Ile Arg Phe Val Asn Val Phe Lys Asp Lys Thr Leu 1765 1770 1775	5328
GCA AAT AAG CTA TCT TTT AAC TTT AGT GAT AAA CAA GAT GTA CCT GTA Ala Asn Lys Leu Ser Phe Asn Phe Ser Asp Lys Gln Asp Val Pro Val 1780 1785 1790	5376
AGT GAA ATA ATC TTA TCA TTT ACA CCT TCA TAT TAT GAG GAT GGA TTG Ser Glu Ile Ile Leu Ser Phe Thr Pro Ser Tyr Tyr Glu Asp Gly Leu 1795 1800 1805	5424
ATT GGC TAT GAT TTG GGT CTA GTT TCT TTA TAT AAT GAG AAA TTT TAT Ile Gly Tyr Asp Leu Gly Leu Val Ser Leu Tyr Asn Glu Lys Phe Tyr 1810 1815 1820	5472
ATT AAT AAC TTT GGA ATG ATG GTA TCT GGA TTA ATA TAT ATT AAT GAT Ile Asn Asn Phe Gly Met Met Val Ser Gly Leu Ile Tyr Ile Asn Asp 1825 1830 1835 1840	5520
TCA TTA TAT TAT TTT AAA CCA CCA GTA AAT AAT TTG ATA ACT GGA TTT Ser Leu Tyr Tyr Phe Lys Pro Pro Val Asn Asn Leu Ile Thr Gly Phe 1845 1850 1855	5568
GTG ACT GTA GGC GAT GAT AAA TAC TAC TTT AAT CCA ATT AAT GGT GGA Val Thr Val Gly Asp Asp Lys Tyr Tyr Phe Asn Pro Ile Asn Gly Gly 1860 1865 1870	5616
GCT GCT TCA ATT GGA GAG ACA ATA ATT GAT GAC AAA AAT TAT TAT TTC Ala Ala Ser Ile Gly Glu Thr Ile Ile Asp Asp Lys Asn Tyr Tyr Phe 1875 1880 1885	5664
AAC CAA AGT GGA GTG TTA CAA ACA GGT GTA TTT AGT ACA GAA GAT GGA Asn Gln Ser Gly Val Leu Gln Thr Gly Val Phe Ser Thr Glu Asp Gly 1890 1895 1900	5712
TTT AAA TAT TTT GCC CCA GCT AAT ACA CTT GAT GAA AAC CTA GAA GGA Phe Lys Tyr Phe Ala Pro Ala Asn Thr Leu Asp Glu Asn Leu Glu Gly 1905 1910 1915 1920	5760
GAA GCA ATT GAT TTT ACT GGA AAA TTA ATT ATT GAC GAA AAT ATT TAT Glu Ala Ile Asp Phe Thr Gly Lys Leu Ile Ile Asp Glu Asn Ile Tyr 1925 1930 1935	5808
TAT TTT GAT GAT AAT TAT AGA GGA GCT GTA GAA TGG AAA GAA TTA GAT Tyr Phe Asp Asp Asn Tyr Arg Gly Ala Val Glu Trp Lys Glu Leu Asp 1940 1945 1950	5856
GGT GAA ATG CAC TAT TTT AGC CCA GAA ACA GGT AAA GCT TTT AAA GGT Gly Glu Met His Tyr Phe Ser Pro Glu Thr Gly Lys Ala Phe Lys Gly 1955 1960 1965	5904

CTA AAT CAA ATA GGT GAT TAT AAA TAC TAT TTC AAT TCT GAT GGA GTT Leu Asn Gln Ile Gly Asp Tyr Lys Tyr Tyr Phe Asn Ser Asp Gly Val 1970 1975 1980	5952
ATG CAA AAA GGA TTT GTT AGT ATA AAT GAT AAT AAA CAC TAT TTT GAT Met Gln Lys Gly Phe Val Ser Ile Asn Asp Asn Lys His Tyr Phe Asp 1985 1990 1995 2000	6000
GAT TCT GGT GTT ATG AAA GTA GGT TAC ACT GAA ATA GAT GGC AAG CAT Asp Ser Gly Val Met Lys Val Gly Tyr Thr Glu Ile Asp Gly Lys His 2005 2010 2015	6048
TTC TAC TTT GCT GAA AAC GGA GAA ATG CAA ATA GGA GTA TTT AAT ACA Phe Tyr Phe Ala Glu Asn Gly Glu Met Gln Ile Gly Val Phe Asn Thr 2020 2025 2030	6096
GAA GAT GGA TTT AAA TAT TTT GCT CAT CAT AAT GAA GAT TTA GGA AAT Glu Asp Gly Phe Lys Tyr Phe Ala His His Asn Glu Asp Leu Gly Asn 2035 2040 2045	6144
GAA GAA GGT GAA GAA ATC TCA TAT TCT GGT ATA TTA AAT TTC AAT AAT Glu Glu Gly Glu Glu Ile Ser Tyr Ser Gly Ile Leu Asn Phe Asn Asn 2050 2055 2060	6192
AAA ATT TAC TAT TTT GAT GAT TCA TTT ACA GCT GTA GTT GGA TGG AAA Lys Ile Tyr Tyr Phe Asp Asp Ser Phe Thr Ala Val Val Gly Trp Lys 2065 2070 2075 2080	6240
GAT TTA GAG GAT GGT TCA AAG TAT TAT TTT GAT GAA GAT ACA GCA GAA Asp Leu Glu Asp Gly Ser Lys Tyr Tyr Phe Asp Glu Asp Thr Ala Glu 2085 2090 2095	6288
GCA TAT ATA GGT TTG TCA TTA ATA AAT GAT GGT CAA TAT TAT TTT AAT Ala Tyr Ile Gly Leu Ser Leu Ile Asn Asp Gly Gln Tyr Tyr Phe Asn 2100 2105 2110	6336
GAT GAT GGA ATT ATG CAA GTT GGA TTT GTC ACT ATA AAT GAT AAA GTC Asp Asp Gly Ile Met Gln Val Gly Phe Val Thr Ile Asn Asp Lys Val 2115 2120 2125	6384
TTC TAC TTC TCT GAC TCT GGA ATT ATA GAA TCT GGA GTA CAA AAC ATA Phe Tyr Phe Ser Asp Ser Gly Ile Ile Glu Ser Gly Val Gln Asn Ile 2130 2135 2140	6432
GAT GAC AAT TAT TTC TAT ATA GAT GAT AAT GGT ATA GTT CAA ATT GGT Asp Asp Asn Tyr Phe Tyr Ile Asp Asp Asn Gly Ile Val Gln Ile Gly 2145 2150 2155 2160	6480
GTA TTT GAT ACT TCA GAT GGA TAT AAA TAT TTT GCA CCT GCT AAT ACT Val Phe Asp Thr Ser Asp Gly Tyr Lys Tyr Phe Ala Pro Ala Asn Thr 2165 2170 2175	6528
GTA AAT GAT AAT ATT TAC GGA CAA GCA GTT GAA TAT AGT GGT TTA GTT Val Asn Asp Asn Ile Tyr Gly Gln Ala Val Glu Tyr Ser Gly Leu Val 2180 2185 2190	6576
AGA GTT GGG GAA GAT GTA TAT TAT TTT GGA GAA ACA TAT ACA ATT GAG Arg Val Gly Glu Asp Val Tyr Tyr Phe Gly Glu Thr Tyr Thr Ile Glu 2195 2200 2205	6624

ACT GGA TGG ATA TAT GAT ATG GAA AAT GAA AGT GAT AAA TAT TAT TTC Thr Gly Trp Ile Tyr Asp Met Glu Asn Glu Ser Asp Lys Tyr Tyr Phe 2210 2215 2220	6672
AAT CCA GAA ACT AAA AAA GCA TGC AAA GGT ATT AAT TTA ATT GAT GAT Asn Pro Glu Thr Lys Lys Ala Cys Lys Gly Ile Asn Leu Ile Asp Asp 2225 2230 2235 2240	6720
ATA AAA TAT TAT TTT GAT GAG AAG GGC ATA ATG AGA ACG GGT CTT ATA Ile Lys Tyr Tyr Phe Asp Glu Lys Gly Ile Met Arg Thr Gly Leu Ile 2245 2250 2255	6768
TCA TTT GAA AAT AAT TAC TTT AAT GAG AAT GGT GAA ATG CAA Ser Phe Glu Asn Asn Tyr Tyr Phe Asn Glu Asn Gly Glu Met Gln 2260 2265 2270	6816
TTT GGT TAT ATA AAT ATA GAA GAT AAG ATG TTC TAT TTT GGT GAA GAT Phe Gly Tyr Ile Asn Ile Glu Asp Lys Met Phe Tyr Phe Gly Glu Asp 2275 2280 2285	6864
GGT GTC ATG CAG ATT GGA GTA TTT AAT ACA CCA GAT GGA TTT AAA TAC Gly Val Met Gln Ile Gly Val Phe Asn Thr Pro Asp Gly Phe Lys Tyr 2290 2295 2300	6912
TTT GCA CAT CAA AAT ACT TTG GAT GAG AAT TTT GAG GGA GAA TCA ATA Phe Ala His Gln Asn Thr Leu Asp Glu Asn Phe Glu Gly Glu Ser Ile 2305 2310 2315 2320	6960
AAC TAT ACT GGT TGG TTA GAT TTA GAT GAA AAG AGA TAT TAT TTT ACA Asn Tyr Thr Gly Trp Leu Asp Leu Asp Glu Lys Arg Tyr Tyr Phe Thr 2325 2330 2335	7008
GAT GAA TAT ATT GCA GCA ACT GGT TCA GTT ATT ATT GAT GGT GAG GAG Asp Glu Tyr Ile Ala Ala Thr Gly Ser Val Ile Ile Asp Gly Glu Glu 2340 2345 2350	7056
TAT TAT TTT GAT CCT GAT ACA GCT CAA TTA GTG ATT AGT GAA Tyr Tyr Phe Asp Pro Asp Thr Ala Gln Leu Val Ile Ser Glu 2355 2360 2365	7098
TAG	7101

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2366 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Leu Val Asn Arg Lys Gln Leu Glu Lys Met Ala Asn Val Arg 1 5 10 15
Phe Arg Thr Gln Glu Asp Glu Tyr Val Ala Ile Leu Asp Ala Leu Glu 20 25 30
Glu Tyr His Asn Met Ser Glu Asn Thr Val Val Glu Lys Tyr Leu Lys 35 40 45

Leu Lys Asp Ile Asn Ser Leu Thr Asp Ile Tyr Ile Asp Thr Tyr Lys  
50 55 60

Lys Ser Gly Arg Asn Lys Ala Leu Lys Lys Phe Lys Glu Tyr Leu Val  
65 70 75 80

Thr Glu Val Leu Glu Leu Lys Asn Asn Asn Leu Thr Pro Val Glu Lys  
85 90 95

Asn Leu His Phe Val Trp Ile Gly Gly Gln Ile Asn Asp Thr Ala Ile  
100 105 110

Asn Tyr Ile Asn Gln Trp Lys Asp Val Asn Ser Asp Tyr Asn Val Asn  
115 120 125

Val Phe Tyr Asp Ser Asn Ala Phe Leu Ile Asn Thr Leu Lys Lys Thr  
130 135 140

Val Val Glu Ser Ala Ile Asn Asp Thr Leu Glu Ser Phe Arg Glu Asn  
145 150 155 160

Leu Asn Asp Pro Arg Phe Asp Tyr Asn Lys Phe Phe Arg Lys Arg Met  
165 170 175

Glu Ile Ile Tyr Asp Lys Gln Lys Asn Phe Ile Asn Tyr Tyr Lys Ala  
180 185 190

Gln Arg Glu Glu Asn Pro Glu Leu Ile Ile Asp Asp Ile Val Lys Thr  
195 200 205

Tyr Leu Ser Asn Glu Tyr Ser Lys Glu Ile Asp Glu Leu Asn Thr Tyr  
210 215 220

Ile Glu Glu Ser Leu Asn Lys Ile Thr Gln Asn Ser Gly Asn Asp Val  
225 230 235 240

Arg Asn Phe Glu Glu Phe Lys Asn Gly Glu Ser Phe Asn Leu Tyr Glu  
245 250 255

Gln Glu Leu Val Glu Arg Trp Asn Leu Ala Ala Ala Ser Asp Ile Leu  
260 265 270

Arg Ile Ser Ala Leu Lys Glu Ile Gly Gly Met Tyr Leu Asp Val Asp  
275 280 285

Met Leu Pro Gly Ile Gln Pro Asp Leu Phe Glu Ser Ile Glu Lys Pro  
290 295 300

Ser Ser Val Thr Val Asp Phe Trp Glu Met Thr Lys Leu Glu Ala Ile  
305 310 315 320

Met Lys Tyr Lys Glu Tyr Ile Pro Glu Tyr Thr Ser Glu His Phe Asp  
325 330 335

Met Leu Asp Glu Glu Val Gln Ser Ser Phe Glu Ser Val Leu Ala Ser  
340 345 350

Lys Ser Asp Lys Ser Glu Ile Phe Ser Ser Leu Gly Asp Met Glu Ala  
355 360 365

Ser Pro Leu Glu Val Lys Ile Ala Phe Asn Ser Lys Gly Ile Ile Asn  
370 375 380

Gln Gly Leu Ile Ser Val Lys Asp Ser Tyr Cys Ser Asn Leu Ile Val  
385 390 395 400

Lys Gln Ile Glu Asn Arg Tyr Lys Ile Leu Asn Asn Ser Leu Asn Pro  
405 410 415

Ala Ile Ser Glu Asp Asn Asp Phe Asn Thr Thr Thr Asn Thr Phe Ile  
420 425 430

Asp Ser Ile Met Ala Glu Ala Asn Ala Asp Asn Gly Arg Phe Met Met  
435 440 445

Glu Leu Gly Lys Tyr Leu Arg Val Gly Phe Phe Pro Asp Val Lys Thr  
450 455 460

Thr Ile Asn Leu Ser Gly Pro Glu Ala Tyr Ala Ala Ala Tyr Gln Asp  
465 470 475 480

Leu Leu Met Phe Lys Glu Gly Ser Met Asn Ile His Leu Ile Glu Ala  
485 490 495

Asp Leu Arg Asn Phe Glu Ile Ser Lys Thr Asn Ile Ser Gln Ser Thr  
500 505 510

Glu Gln Glu Met Ala Ser Leu Trp Ser Phe Asp Asp Ala Arg Ala Lys  
515 520 525

Ala Gln Phe Glu Glu Tyr Lys Arg Asn Tyr Phe Glu Gly Ser Leu Gly  
530 535 540

Glu Asp Asp Asn Leu Asp Phe Ser Gln Asn Ile Val Val Asp Lys Glu  
545 550 555 560

Tyr Leu Leu Glu Lys Ile Ser Ser Leu Ala Arg Ser Ser Glu Arg Gly  
565 570 575

Tyr Ile His Tyr Ile Val Gln Leu Gln Gly Asp Lys Ile Ser Tyr Glu  
580 585 590

Ala Ala Cys Asn Leu Phe Ala Lys Thr Pro Tyr Asp Ser Val Leu Phe  
595 600 605

Gln Lys Asn Ile Glu Asp Ser Glu Ile Ala Tyr Tyr Tyr Asn Pro Gly  
610 615 620

Asp Gly Glu Ile Gln Glu Ile Asp Lys Tyr Lys Ile Pro Ser Ile Ile  
625 630 635 640

Ser Asp Arg Pro Lys Ile Lys Leu Thr Phe Ile Gly His Gly Lys Asp  
645 650 655

Glu Phe Asn Thr Asp Ile Phe Ala Gly Phe Asp Val Asp Ser Leu Ser  
660 665 670

Thr Glu Ile Glu Ala Ala Ile Asp Leu Ala Lys Glu Asp Ile Ser Pro  
675 680 685

Lys Ser Ile Glu Ile Asn Leu Leu Gly Cys Asn Met Phe Ser Tyr Ser  
690 695 700

Ile Asn Val Glu Glu Thr Tyr Pro Gly Lys Leu Leu Leu Lys Val Lys  
705 710 715 720

ASP Lys Ile Ser Glu Leu Met Pro Ser Ile Ser Gln Asp Ser Ile Ile  
 725 730 735  
 Val Ser Ala Asn Gln Tyr Glu Val Arg Ile Asn Ser Glu Gly Arg Arg  
 740 745 750  
 Glu Leu Leu Asp His Ser Gly Glu Trp Ile Asn Lys Glu Glu Ser Ile  
 755 760 765  
 Ile Lys Asp Ile Ser Ser Lys Glu Tyr Ile Ser Phe Asn Pro Lys Glu  
 770 775 780  
 Asn Lys Ile Thr Val Lys Ser Lys Asn Leu Pro Glu Leu Ser Thr Leu  
 785 790 795 800  
 Leu Gln Glu Ile Arg Asn Asn Ser Asn Ser Ser Asp Ile Glu Leu Glu  
 805 810 815  
 Glu Lys Val Met Leu Thr Glu Cys Glu Ile Asn Val Ile Ser Asn Ile  
 820 825 830  
 Asp Thr Gln Ile Val Glu Glu Arg Ile Glu Glu Ala Lys Asn Leu Thr  
 835 840 845  
 Ser Asp Ser Ile Asn Tyr Ile Lys Asp Glu Phe Lys Leu Ile Glu Ser  
 850 855 860  
 Ile Ser Asp Ala Leu Cys Asp Leu Lys Gln Gln Asn Glu Leu Glu Asp  
 865 870 875 880  
 Ser His Phe Ile Ser Phe Glu Asp Ile Ser Glu Thr Asp Glu Gly Phe  
 885 890 895  
 Ser Ile Arg Phe Ile Asn Lys Glu Thr Gly Glu Ser Ile Phe Val Glu  
 900 905 910  
 Thr Glu Lys Thr Ile Phe Ser Glu Tyr Ala Asn His Ile Thr Glu Glu  
 915 920 925  
 Ile Ser Lys Ile Lys Gly Thr Ile Phe Asp Thr Val Asn Gly Lys Leu  
 930 935 940  
 Val Lys Lys Val Asn Leu Asp Thr Thr His Glu Val Asn Thr Leu Asn  
 945 950 955 960  
 Ala Ala Phe Phe Ile Gln Ser Leu Ile Glu Tyr Asn Ser Ser Lys Glu  
 965 970 975  
 Ser Leu Ser Asn Leu Ser Val Ala Met Lys Val Gln Val Tyr Ala Gln  
 980 985 990  
 Leu Phe Ser Thr Gly Leu Asn Thr Ile Thr Asp Ala Ala Lys Val Val  
 995 1000 1005  
 Glu Leu Val Ser Thr Ala Leu Asp Glu Thr Ile Asp Leu Leu Pro Thr  
 1010 1015 1020  
 Leu Ser Glu Gly Leu Pro Ile Ile Ala Thr Ile Ile Asp Gly Val Ser  
 1025 1030 1035 1040  
 Leu Gly Ala Ala Ile Lys Glu Leu Ser Glu Thr Ser Asp Pro Leu Leu  
 1045 1050 1055

Arg Gln Glu Ile Glu Ala Lys Ile Gly Ile Met Ala Val Asn Leu Thr  
 1060 1065 1070  
 Thr Ala Thr Thr Ala Ile Ile Thr Ser Ser Leu Gly Ile Ala Ser Gly  
 1075 1080 1085  
 Phe Ser Ile Leu Leu Val Pro Leu Ala Gly Ile Ser Ala Gly Ile Pro  
 1090 1095 1100  
 Ser Leu Val Asn Asn Glu Leu Val Leu Arg Asp Lys Ala Thr Lys Val  
 1105 1110 1115 1120  
 Val Asp Tyr Phe Lys His Val Ser Leu Val Glu Thr Glu Gly Val Phe  
 1125 1130 1135  
 Thr Leu Leu Asp Asp Lys Ile Met Met Pro Gln Asp Asp Leu Val Ile  
 1140 1145 1150  
 Ser Glu Ile Asp Phe Asn Asn Asn Ser Ile Val Leu Gly Lys Cys Glu  
 1155 1160 1165  
 Ile Trp Arg Met Glu Gly Gly Ser Gly His Thr Val Thr Asp Asp Ile  
 1170 1175 1180  
 Asp His Phe Phe Ser Ala Pro Ser Ile Thr Tyr Arg Glu Pro His Leu  
 1185 1190 1195 1200  
 Ser Ile Tyr Asp Val Leu Glu Val Gln Lys Glu Glu Leu Asp Leu Ser  
 1205 1210 1215  
 Lys Asp Leu Met Val Leu Pro Asn Ala Pro Asn Arg Val Phe Ala Trp  
 1220 1225 1230  
 Glu Thr Gly Trp Thr Pro Gly Leu Arg Ser Leu Glu Asn Asp Gly Thr  
 1235 1240 1245  
 Lys Leu Leu Asp Arg Ile Arg Asp Asn Tyr Glu Gly Glu Phe Tyr Trp  
 1250 1255 1260  
 Arg Tyr Phe Ala Phe Ile Ala Asp Ala Leu Ile Thr Thr Leu Lys Pro  
 1265 1270 1275 1280  
 Arg Tyr Glu Asp Thr Asn Ile Arg Ile Asn Leu Asp Ser Asn Thr Arg  
 1285 1290 1295  
 Ser Phe Ile Val Pro Ile Ile Thr Thr Glu Tyr Ile Arg Glu Lys Leu  
 1300 1305 1310  
 Ser Tyr Ser Phe Tyr Gly Ser Gly Gly Thr Tyr Ala Leu Ser Leu Ser  
 1315 1320 1325  
 Gln Tyr Asn Met Gly Ile Asn Ile Glu Leu Ser Glu Ser Asp Val Trp  
 1330 1335 1340  
 Ile Ile Asp Val Asp Asn Val Val Arg Asp Val Thr Ile Glu Ser Asp  
 1345 1350 1355 1360  
 Lys Ile Lys Lys Gly Asp Leu Ile Glu Gly Ile Leu Ser Thr Leu Ser  
 1365 1370 1375  
 Ile Glu Glu Asn Lys Ile Ile Leu Asn Ser His Glu Ile Asn Phe Ser  
 1380 1385 1390

Gly Glu Val Asn Gly Ser Asn Gly Phe Val Ser Leu Thr Phe Ser Ile  
1395 1400 1405

Leu Glu Gly Ile Asn Ala Ile Ile Glu Val Asp Leu Leu Ser Lys Ser  
1410 1415 1420

Tyr Lys Leu Leu Ile Ser Gly Glu Leu Lys Ile Leu Met Leu Asn Ser  
1425 1430 1435 1440

Asn His Ile Gln Gln Lys Ile Asp Tyr Ile Gly Phe Asn Ser Glu Leu  
1445 1450 1455

Gln Lys Asn Ile Pro Tyr Ser Phe Val Asp Ser Glu Gly Lys Glu Asn  
1460 1465 1470

Gly Phe Ile Asn Gly Ser Thr Lys Glu Gly Leu Phe Val Ser Glu Leu  
1475 1480 1485

Pro Asp Val Val Leu Ile Ser Lys Val Tyr Met Asp Asp Ser Lys Pro  
1490 1495 1500

Ser Phe Gly Tyr Tyr Ser Asn Asn Leu Lys Asp Val Lys Val Ile Thr  
1505 1510 1515 1520

Lys Asp Asn Val Asn Ile Leu Thr Gly Tyr Tyr Leu Lys Asp Asp Ile  
1525 1530 1535

Lys Ile Ser Leu Ser Leu Thr Leu Gln Asp Glu Lys Thr Ile Lys Leu  
1540 1545 1550

Asn Ser Val His Leu Asp Glu Ser Gly Val Ala Glu Ile Leu Lys Phe  
1555 1560 1565

Met Asn Arg Lys Gly Asn Thr Asn Thr Ser Asp Ser Leu Met Ser Phe  
1570 1575 1580

Leu Glu Ser Met Asn Ile Lys Ser Ile Phe Val Asn Phe Leu Gln Ser  
1585 1590 1595 1600

Asn Ile Lys Phe Ile Leu Asp Ala Asn Phe Ile Ile Ser Gly Thr Thr  
1605 1610 1615

Ser Ile Gly Gln Phe Glu Phe Ile Cys Asp Glu Asn Asp Asn Ile Gln  
1620 1625 1630

Pro Tyr Phe Ile Lys Phe Asn Thr Leu Glu Thr Asn Tyr Thr Leu Tyr  
1635 1640 1645

Val Gly Asn Arg Gln Asn Met Ile Val Glu Pro Asn Tyr Asp Leu Asp  
1650 1655 1660

Asp Ser Gly Asp Ile Ser Ser Thr Val Ile Asn Phe Ser Gln Lys Tyr  
1665 1670 1675 1680

Leu Tyr Gly Ile Asp Ser Cys Val Asn Lys Val Val Ile Ser Pro Asn  
1685 1690 1695

Ile Tyr Thr Asp Glu Ile Asn Ile Thr Pro Val Tyr Glu Thr Asn Asn  
1700 1705 1710

Thr Tyr Pro Glu Val Ile Val Leu Asp Ala Asn Tyr Ile Asn Glu Lys  
1715 1720 1725

Ile Asn Val Asn Ile Asn Asp Leu Ser Ile Arg Tyr Val Trp Ser Asn  
 1730 1735 1740  
 Asp Gly Asn Asp Phe Ile Leu Met Ser Thr Ser Glu Glu Asn Lys Val  
 1745 1750 1755 1760  
 Ser Gln Val Lys Ile Arg Phe Val Asn Val Phe Lys Asp Lys Thr Leu  
 1765 1770 1775  
 Ala Asn Lys Leu Ser Phe Asn Phe Ser Asp Lys Gln Asp Val Pro Val  
 1780 1785 1790  
 Ser Glu Ile Ile Leu Ser Phe Thr Pro Ser Tyr Tyr Glu Asp Gly Leu  
 1795 1800 1805  
 Ile Gly Tyr Asp Leu Gly Leu Val Ser Leu Tyr Asn Glu Lys Phe Tyr  
 1810 1815 1820  
 Ile Asn Asn Phe Gly Met Met Val Ser Gly Leu Ile Tyr Ile Asn Asp  
 1825 1830 1835 1840  
 Ser Leu Tyr Tyr Phe Lys Pro Pro Val Asn Asn Leu Ile Thr Gly Phe  
 1845 1850 1855  
 Val Thr Val Gly Asp Asp Lys Tyr Tyr Phe Asn Pro Ile Asn Gly Gly  
 1860 1865 1870  
 Ala Ala Ser Ile Gly Glu Thr Ile Ile Asp Asp Lys Asn Tyr Tyr Phe  
 1875 1880 1885  
 Asn Gln Ser Gly Val Leu Gln Thr Gly Val Phe Ser Thr Glu Asp Gly  
 1890 1895 1900  
 Phe Lys Tyr Phe Ala Pro Ala Asn Thr Leu Asp Glu Asn Leu Glu Gly  
 1905 1910 1915 1920  
 Glu Ala Ile Asp Phe Thr Gly Lys Leu Ile Ile Asp Glu Asn Ile Tyr  
 1925 1930 1935  
 Tyr Phe Asp Asp Asn Tyr Arg Gly Ala Val Glu Trp Lys Glu Leu Asp  
 1940 1945 1950  
 Gly Glu Met His Tyr Phe Ser Pro Glu Thr Gly Lys Ala Phe Lys Gly  
 1955 1960 1965  
 Leu Asn Gln Ile Gly Asp Tyr Lys Tyr Tyr Phe Asn Ser Asp Gly Val  
 1970 1975 1980  
 Met Gln Lys Gly Phe Val Ser Ile Asn Asp Asn Lys His Tyr Phe Asp  
 1985 1990 1995 2000  
 Asp Ser Gly Val Met Lys Val Gly Tyr Thr Glu Ile Asp Gly Lys His  
 2005 2010 2015  
 Phe Tyr Phe Ala Glu Asn Gly Glu Met Gln Ile Gly Val Phe Asn Thr  
 2020 2025 2030  
 Glu Asp Gly Phe Lys Tyr Phe Ala His His Asn Glu Asp Leu Gly Asn  
 2035 2040 2045  
 Glu Glu Gly Glu Glu Ile Ser Tyr Ser Gly Ile Leu Asn Phe Asn Asn  
 2050 2055 2060

Lys Ile Tyr Tyr Phe Asp Asp Ser Phe Thr Ala Val Val Gly Trp Lys  
2065 2070 2075 2080

Asp Leu Glu Asp Gly Ser Lys Tyr Tyr Phe Asp Glu Asp Thr Ala Glu  
2085 2090 2095

Ala Tyr Ile Gly Leu Ser Leu Ile Asn Asp Gly Gln Tyr Tyr Phe Asn  
2100 2105 2110

Asp Asp Gly Ile Met Gln Val Gly Phe Val Thr Ile Asn Asp Lys Val  
2115 2120 2125

Phe Tyr Phe Ser Asp Ser Gly Ile Ile Glu Ser Gly Val Gln Asn Ile  
2130 2135 2140

Asp Asp Asn Tyr Phe Tyr Ile Asp Asp Asn Gly Ile Val Gln Ile Gly  
2145 2150 2155 2160

Val Phe Asp Thr Ser Asp Gly Tyr Lys Tyr Phe Ala Pro Ala Asn Thr  
2165 2170 2175

Val Asn Asp Asn Ile Tyr Gly Gln Ala Val Glu Tyr Ser Gly Leu Val  
2180 2185 2190

Arg Val Gly Glu Asp Val Tyr Tyr Phe Gly Glu Thr Tyr Thr Ile Glu  
2195 2200 2205

Thr Gly Trp Ile Tyr Asp Met Glu Asn Glu Ser Asp Lys Tyr Tyr Phe  
2210 2215 2220

Asn Pro Glu Thr Lys Lys Ala Cys Lys Gly Ile Asn Leu Ile Asp Asp  
2225 2230 2235 2240

Ile Lys Tyr Tyr Phe Asp Glu Lys Gly Ile Met Arg Thr Gly Leu Ile  
2245 2250 2255

Ser Phe Glu Asn Asn Asn Tyr Tyr Phe Asn Glu Asn Gly Glu Met Gln  
2260 2265 2270

Phe Gly Tyr Ile Asn Ile Glu Asp Lys Met Phe Tyr Phe Gly Glu Asp  
2275 2280 2285

Gly Val Met Gln Ile Gly Val Phe Asn Thr Pro Asp Gly Phe Lys Tyr  
2290 2295 2300

Phe Ala His Gln Asn Thr Leu Asp Glu Asn Phe Glu Gly Glu Ser Ile  
2305 2310 2315 2320

Asn Tyr Thr Gly Trp Leu Asp Leu Asp Glu Lys Arg Tyr Tyr Phe Thr  
2325 2330 2335

Asp Glu Tyr Ile Ala Ala Thr Gly Ser Val Ile Ile Asp Gly Glu Glu  
2340 2345 2350

Tyr Tyr Phe Asp Pro Asp Thr Ala Gln Leu Val Ile Ser Glu  
2355 2360 2365

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TAGAAAAAAAT GGCAAATGT

19

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTCATCTTG TAGAGTCAAA G

21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATGCCACAA GATGATTTAG TG

22

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTAATTGAGC TGTATCAGGA TC

22

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGGAATTCCCT AGAAAAATG GCAAATG

27

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCTCTAGAAC GACCATAAGC TAGCCA

26

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGGAATTCGA GTTGGTAGAA AGGTGGA

27

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGGAATTCCGG TTATTATCTT AAGGATG

27

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CGGAATTCTT GATAACTGGA TTTGTGAC

28

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 511 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Leu Ile Thr Gly Phe Val Thr Val Gly Asp Asp Lys Tyr Tyr Phe Asn  
1 5 10 15

Pro Ile Asn Gly Gly Ala Ala Ser Ile Gly Glu Thr Ile Ile Asp Asp  
20 25 30

Lys Asn Tyr Tyr Phe Asn Gln Ser Gly Val Leu Gln Thr Gly Val Phe  
35 40 45

Ser Thr Glu Asp Gly Phe Lys Tyr Phe Ala Pro Ala Asn Thr Leu Asp  
50 55 60

Glu Asn Leu Glu Gly Glu Ala Ile Asp Phe Thr Gly Lys Leu Ile Ile  
65 70 75 80

Asp Glu Asn Ile Tyr Tyr Phe Asp Asp Asn Tyr Arg Gly Ala Val Glu  
85 90 95

Trp Lys Glu Leu Asp Gly Glu Met His Tyr Phe Ser Pro Glu Thr Gly  
100 105 110

Lys Ala Phe Lys Gly Leu Asn Gln Ile Gly Asp Tyr Lys Tyr Tyr Phe  
115 120 125

Asn Ser Asp Gly Val Met Gln Lys Gly Phe Val Ser Ile Asn Asp Asn  
130 135 140

Lys His Tyr Phe Asp Asp Ser Gly Val Met Lys Val Gly Tyr Thr Glu  
145 150 155 160

Ile Asp Gly Lys His Phe Tyr Phe Ala Glu Asn Gly Glu Met Gln Ile  
165 170 175

Gly Val Phe Asn Thr Glu Asp Gly Phe Lys Tyr Phe Ala His His Asn  
180 185 190

Glu Asp Leu Gly Asn Glu Glu Gly Glu Glu Ile Ser Tyr Ser Gly Ile  
 195 200 205  
 Leu Asn Phe Asn Asn Lys Ile Tyr Tyr Phe Asp Asp Ser Phe Thr Ala  
 210 215 220  
 Val Val Gly Trp Lys Asp Leu Glu Asp Gly Ser Lys Tyr Tyr Phe Asp  
 225 230 235 240  
 Glu Asp Thr Ala Glu Ala Tyr Ile Gly Leu Ser Leu Ile Asn Asp Gly  
 245 250 255  
 Gln Tyr Tyr Phe Asn Asp Asp Gly Ile Met Gln Val Gly Phe Val Thr  
 260 265 270  
 Ile Asn Asp Lys Val Phe Tyr Phe Ser Asp Ser Gly Ile Ile Glu Ser  
 275 280 285  
 Gly Val Gln Asn Ile Asp Asp Asn Tyr Phe Tyr Ile Asp Asp Asn Gly  
 290 295 300  
 Ile Val Gln Ile Gly Val Phe Asp Thr Ser Asp Gly Tyr Lys Tyr Phe  
 305 310 315 320  
 Ala Pro Ala Asn Thr Val Asn Asp Asn Ile Tyr Gly Gln Ala Val Glu  
 325 330 335  
 Tyr Ser Gly Leu Val Arg Val Gly Glu Asp Val Tyr Tyr Phe Gly Glu  
 340 345 350  
 Thr Tyr Thr Ile Glu Thr Gly Trp Ile Tyr Asp Met Glu Asn Glu Ser  
 355 360 365  
 Asp Lys Tyr Tyr Phe Asn Pro Glu Thr Lys Lys Ala Cys Lys Gly Ile  
 370 375 380  
 Asn Leu Ile Asp Asp Ile Lys Tyr Tyr Phe Asp Glu Lys Gly Ile Met  
 385 390 395 400  
 Arg Thr Gly Leu Ile Ser Phe Glu Asn Asn Asn Tyr Tyr Phe Asn Glu  
 405 410 415  
 Asn Gly Glu Met Gln Phe Gly Tyr Ile Asn Ile Glu Asp Lys Met Phe  
 420 425 430  
 Tyr Phe Gly Glu Asp Gly Val Met Gln Ile Gly Val Phe Asn Thr Pro  
 435 440 445  
 Asp Gly Phe Lys Tyr Phe Ala His Gln Asn Thr Leu Asp Glu Asn Phe  
 450 455 460  
 Glu Gly Glu Ser Ile Asn Tyr Thr Gly Trp Leu Asp Leu Asp Glu Lys  
 465 470 475 480  
 Arg Tyr Tyr Phe Thr Asp Glu Tyr Ile Ala Ala Thr Gly Ser Val Ile  
 485 490 495  
 Ile Asp Gly Glu Glu Tyr Tyr Phe Asp Pro Asp Thr Ala Gln Leu  
 500 505 510

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 608 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ser Glu Glu Asn Lys Val Ser Gln Val Lys Ile Arg Phe Val Asn Val  
1 5 10 15

Phe Lys Asp Lys Thr Leu Ala Asn Lys Leu Ser Phe Asn Phe Ser Asp  
20 25 30

Lys Gln Asp Val Pro Val Ser Glu Ile Ile Leu Ser Phe Thr Pro Ser  
35 40 45

Tyr Tyr Glu Asp Gly Leu Ile Gly Tyr Asp Leu Gly Leu Val Ser Leu  
50 55 60

Tyr Asn Glu Lys Phe Tyr Ile Asn Asn Phe Gly Met Met Val Ser Gly  
65 70 75 80

Leu Ile Tyr Ile Asn Asp Ser Leu Tyr Tyr Phe Lys Pro Pro Val Asn  
85 90 95

Asn Leu Ile Thr Gly Phe Val Thr Val Gly Asp Asp Lys Tyr Tyr Phe  
100 105 110

Asn Pro Ile Asn Gly Gly Ala Ala Ser Ile Gly Glu Thr Ile Ile Asp  
115 120 125

Asp Lys Asn Tyr Tyr Phe Asn Gln Ser Gly Val Leu Gln Thr Gly Val  
130 135 140

Phe Ser Thr Glu Asp Gly Phe Lys Tyr Phe Ala Pro Ala Asn Thr Leu  
145 150 155 160

Asp Glu Asn Leu Glu Gly Glu Ala Ile Asp Phe Thr Gly Lys Leu Ile  
165 170 175

Ile Asp Glu Asn Ile Tyr Tyr Phe Asp Asp Asn Tyr Arg Gly Ala Val  
180 185 190

Glu Trp Lys Glu Leu Asp Gly Glu Met His Tyr Phe Ser Pro Glu Thr  
195 200 205

Gly Lys Ala Phe Lys Gly Leu Asn Gln Ile Gly Asp Tyr Lys Tyr Tyr  
210 215 220

Phe Asn Ser Asp Gly Val Met Gln Lys Gly Phe Val Ser Ile Asn Asp  
225 230 235 240

Asn Lys His Tyr Phe Asp Asp Ser Gly Val Met Lys Val Gly Tyr Thr  
245 250 255

Glu Ile Asp Gly Lys His Phe Tyr Phe Ala Glu Asn Gly Glu Met Gln  
260 265 270

Ile Gly Val Phe Asn Thr Glu Asp Gly Phe Lys Tyr Phe Ala His His  
 275 280 285  
 Asn Glu Asp Leu Gly Asn Glu Glu Gly Glu Glu Ile Ser Tyr Ser Gly  
 290 295 300  
 Ile Leu Asn Phe Asn Asn Lys Ile Tyr Tyr Phe Asp Asp Ser Phe Thr  
 305 310 315 320  
 Ala Val Val Gly Trp Lys Asp Leu Glu Asp Gly Ser Lys Tyr Tyr Phe  
 325 330 335  
 Asp Glu Asp Thr Ala Glu Ala Tyr Ile Gly Leu Ser Leu Ile Asn Asp  
 340 345 350  
 Gly Gln Tyr Tyr Phe Asn Asp Asp Gly Ile Met Gln Val Gly Phe Val  
 355 360 365  
 Thr Ile Asn Asp Lys Val Phe Tyr Phe Ser Asp Ser Gly Ile Ile Glu  
 370 375 380  
 Ser Gly Val Gln Asn Ile Asp Asp Asn Tyr Phe Tyr Ile Asp Asp Asn  
 385 390 395 400  
 Gly Ile Val Gln Ile Gly Val Phe Asp Thr Ser Asp Gly Tyr Lys Tyr  
 405 410 415  
 Phe Ala Pro Ala Asn Thr Val Asn Asp Asn Ile Tyr Gly Gln Ala Val  
 420 425 430  
 Glu Tyr Ser Gly Leu Val Arg Val Gly Glu Asp Val Tyr Tyr Phe Gly  
 435 440 445  
 Glu Thr Tyr Thr Ile Glu Thr Gly Trp Ile Tyr Asp Met Glu Asn Glu  
 450 455 460  
 Ser Asp Lys Tyr Tyr Phe Asn Pro Glu Thr Lys Lys Ala Cys Lys Gly  
 465 470 475 480  
 Ile Asn Leu Ile Asp Asp Ile Lys Tyr Tyr Phe Asp Glu Lys Gly Ile  
 485 490 495  
 Met Arg Thr Gly Leu Ile Ser Phe Glu Asn Asn Asn Tyr Tyr Phe Asn  
 500 505 510  
 Glu Asn Gly Glu Met Gln Phe Gly Tyr Ile Asn Ile Glu Asp Lys Met  
 515 520 525  
 Phe Tyr Phe Gly Glu Asp Gly Val Met Gln Ile Gly Val Phe Asn Thr  
 530 535 540  
 Pro Asp Gly Phe Lys Tyr Phe Ala His Gln Asn Thr Leu Asp Glu Asn  
 545 550 555 560  
 Phe Glu Gly Glu Ser Ile Asn Tyr Thr Gly Trp Leu Asp Leu Asp Glu  
 565 570 575  
 Lys Arg Tyr Tyr Phe Thr Asp Glu Tyr Ile Ala Ala Thr Gly Ser Val  
 580 585 590  
 Ile Ile Asp Gly Glu Glu Tyr Tyr Phe Asp Pro Asp Thr Ala Gln Leu  
 595 600 605

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATG GCT CGT CTG CTG TCT ACC TTC ACT GAA TAC ATC AAG AAC ATC ATC Met Ala Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile	48
1 5 10 15	
AAT ACC TCC ATC CTG AAC CTG CCG TAC GAA TCC AAT CAC CTG ATC GAC Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp	96
20 25 30	
CTG TCT CGC TAC GCT TCC AAA ATC AAC ATC GGT TCT AAA GTT AAC TTC Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe	144
35 40 45	
GAT CCG ATC GAC AAG AAT CAG ATC CAG CTG TTC AAT CTG GAA TCT TCC Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser	192
50 55 60	
AAA ATC GAA GTT ATC CTG AAG AAT GCT ATC GTA TAC AAC TCT ATG TAC Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr	240
65 70 75 80	
GAA AAC TTC TCC ACC TCC TTC TGG ATC CGT ATC CCG AAA TAC TTC AAC Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn	288
85 90 95	
TCC ATC TCT CTG AAC AAT GAA TAC ACC ATC AAC TGC ATG GAA AAC Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn	336
100 105 110	
AAT TCT GGT TGG AAA GTA TCT CTG AAC TAC GGT GAA ATC ATC TGG ACT Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr	384
115 120 125	
CTG CAG GAC ACT CAG GAA ATC AAA CAG CGT GTT GTA TTC AAA TAC TCT Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser	432
130 135 140	
CAG ATG ATC AAC ATC TCT GAC TAC ATC AAT CGC TGG ATC TTC GTT ACC Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr	480
145 150 155 160	
ATC ACC AAC AAT CGT CTG AAT AAC TCC AAA ATC TAC ATC AAC GGC CGT Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg	528
165 170 175	

CTG ATC GAC CAG AAA CCG ATC TCC AAT CTG GGT AAC ATC CAC GCT TCT Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser 180 185 190	576
AAT AAC ATC ATG TTC AAA CTG GAC GGT TGT CGT GAC ACT CAC CGC TAC Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr 195 200 205	624
ATC TGG ATC AAA TAC TTC AAT CTG TTC GAC AAA GAA CTG AAC GAA AAA Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys 210 215 220	672
GAA ATC AAA GAC CTG TAC GAC AAC CAG TCC AAT TCT GGT ATC CTG AAA Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys 225 230 235 240	720
GAC TTC TGG GGT GAC TAC CTG CAG TAC GAC AAA CCG TAC TAC ATG CTG Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu 245 250 255	768
AAT CTG TAC GAT CCG AAC AAA TAC GTT GAC GTC AAC AAT GTA GGT ATC Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile 260 265 270	816
CGC GGT TAC ATG TAC CTG AAA GGT CCG CGT GGT TCT GTT ATG ACT ACC Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr 275 280 285	864
AAC ATC TAC CTG AAC TCT TCC CTG TAC CGT GGT ACC AAA TTC ATC ATC Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile 290 295 300	912
AAG AAA TAC GCG TCT GGT AAC AAG GAC AAT ATC GTT CGC AAC AAT GAT Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp 305 310 315 320	960
CGT GTA TAC ATC AAT GTT GTA GTT AAG AAC AAA GAA TAC CGT CTG GCT Arg Val Tyr Ile Asn Val Val Lys Asn Lys Glu Tyr Arg Leu Ala 325 330 335	1008
ACC AAT GCT TCT CAG GCT GGT GTA GAA AAG ATC TTG TCT GCT CTG GAA Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu 340 345 350	1056
ATC CCG GAC GTT GGT AAT CTG TCT CAG GTA GTT GTA ATG AAA TCC AAG Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Met Lys Ser Lys 355 360 365	1104
AAC GAC CAG GGT ATC ACT AAC AAA TGC AAA ATG AAT CTG CAG GAC AAC Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn 370 375 380	1152
AAT GGT AAC GAT ATC GGT TTC ATC GGT TTC CAC CAG TTC AAC AAT ATC Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile 385 390 395 400	1200
GCT AAA CTG GTT GCT TCC AAC TGG TAC AAT CGT CAG ATC GAA CGT TCC Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser 405 410 415	1248

TCT CGC ACT CTG GGT TGC TCT TGG GAG TTC ATC CCG GTT GAT GAC GGT  
Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly  
420 425 430

1296

TGG GGT GAA CGT CCG CTG TAACCCGGGA AAGCTT  
Trp Gly Glu Arg Pro Leu  
435

1330

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Ala Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile  
1 5 10 15

Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp  
20 25 30

Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe  
35 40 45

Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser  
50 55 60

Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr  
65 70 75 80

Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn  
85 90 95

Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn  
100 105 110

Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr  
115 120 125

Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser  
130 135 140

Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr  
145 150 155 160

Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg  
165 170 175

Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser  
180 185 190

Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr  
195 200 205

Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys  
210 215 220

Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys  
 225                    230                    235                    240  
 Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu  
 245                    250                    255  
 Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile  
 260                    265                    270  
 Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr  
 275                    280                    285  
 Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile  
 290                    295                    300  
 Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp  
 305                    310                    315                    320  
 Arg Val Tyr Ile Asn Val Val Lys Asn Lys Glu Tyr Arg Leu Ala  
 325                    330                    335  
 Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu  
 340                    345                    350  
 Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys  
 355                    360                    365  
 Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn  
 370                    375                    380  
 Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile  
 385                    390                    395                    400  
 Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser  
 405                    410                    415  
 Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly  
 420                    425                    430  
 Trp Gly Glu Arg Pro Leu  
 435

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Gly His His His His His His His His His Ser Ser Gly His  
 1                    5                    10                    15  
 Ile Glu Gly Arg His Met Ala  
 20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1402 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..1386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATG	GGC	CAT	CAC	AGC	AGC	GGC	CAT		48							
Met	Gly	His	Ser	Ser	Ser	Gly	His									
1		5				10							15			
ATC	GAA	GGT	CGT	CAT	ATG	GCT	AGC	ATG	GCT	CGT	CTG	CTG	TCT	ACC	TTC	96
Ile	Glu	Gly	Arg	His	Met	Ala	Ser	Met	Ala	Arg	Leu	Leu	Ser	Thr	Phe	
	20				25						30					
ACT	GAA	TAC	ATC	AAG	AAC	ATC	ATC	AAT	ACC	TCC	ATC	CTG	AAC	CTG	CGC	144
Thr	Glu	Tyr	Ile	Lys	Asn	Ile	Ile	Asn	Thr	Ser	Ile	Leu	Asn	Leu	Arg	
	35				40						45					
TAC	GAA	TCC	AAT	CAC	CTG	ATC	GAC	CTG	TCT	CGC	TAC	GCT	TCC	AAA	ATC	192
Tyr	Glu	Ser	Asn	His	Leu	Ile	Asp	Leu	Ser	Arg	Tyr	Ala	Ser	Lys	Ile	
	50				55						60					
AAC	ATC	GGT	TCT	AAA	GTT	AAC	TTC	GAT	CCG	ATC	GAC	AAG	AAT	CAG	ATC	240
Asn	Ile	Gly	Ser	Lys	Val	Asn	Phe	Asp	Pro	Ile	Asp	Lys	Asn	Gln	Ile	
	65				70				75					80		
CAG	CTG	TTC	AAT	CTG	GAA	TCT	TCC	AAA	ATC	GAA	GTT	ATC	CTG	AAG	AAT	288
Gln	Leu	Phe	Asn	Leu	Glu	Ser	Ser	Lys	Ile	Glu	Val	Ile	Leu	Lys	Asn	
		85				90						95				
GCT	ATC	GTA	TAC	AAC	TCT	ATG	TAC	GAA	AAC	TTC	TCC	ACC	TCC	TTC	TGG	336
Ala	Ile	Val	Tyr	Asn	Ser	Met	Tyr	Glu	Asn	Phe	Ser	Thr	Ser	Phe	Trp	
		100				105						110				
ATC	CGT	ATC	CCG	AAA	TAC	TTC	AAC	TCC	ATC	TCT	CTG	AAC	AAT	GAA	TAC	384
Ile	Arg	Ile	Pro	Lys	Tyr	Phe	Asn	Ser	Ile	Ser	Leu	Asn	Asn	Glu	Tyr	
	115				120						125					
ACC	ATC	ATC	AAC	TGC	ATG	GAA	AAC	AAT	TCT	GGT	TGG	AAA	GTA	TCT	CTG	432
Thr	Ile	Ile	Asn	Cys	Met	Glu	Asn	Asn	Ser	Gly	Trp	Lys	Val	Ser	Leu	
	130				135						140					
AAC	TAC	GGT	GAA	ATC	ATC	TGG	ACT	CTG	CAG	GAC	ACT	CAG	GAA	ATC	AAA	480
Asn	Tyr	Gly	Glu	Ile	Ile	Trp	Thr	Leu	Gln	Asp	Thr	Gln	Glu	Ile	Lys	
	145				150				155					160		
CAG	CGT	GTT	GTA	TTC	AAA	TAC	TCT	CAG	ATG	ATC	AAC	ATC	TCT	GAC	TAC	528
Gln	Arg	Val	Val	Phe	Lys	Tyr	Ser	Gln	Met	Ile	Asn	Ile	Ser	Asp	Tyr	
		165			170						175					

ATC AAT CGC TGG ATC TTC GTT ACC ATC ACC AAC AAT CGT CTG AAT AAC Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn Asn 180 185 190	576
TCC AAA ATC TAC ATC AAC GGC CGT CTG ATC GAC CAG AAA CCG ATC TCC Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser 195 200 205	624
AAT CTG GGT AAC ATC CAC GCT TCT AAT AAC ATC ATG TTC AAA CTG GAC Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu Asp 210 215 220	672
GGT TGT CGT GAC ACT CAC CGC TAC ATC TGG ATC AAA TAC TTC AAT CTG Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu 225 230 235 240	720
TTC GAC AAA GAA CTG AAC GAA AAA GAA ATC AAA GAC CTG TAC GAC AAC Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn 245 250 255	768
CAG TCC AAT TCT GGT ATC CTG AAA GAC TTC TGG GGT GAC TAC CTG CAG Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln 260 265 270	816
TAC GAC AAA CCG TAC TAC ATG CTG AAT CTG TAC GAT CCG AAC AAA TAC Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr 275 280 285	864
GTT GAC GTC AAC AAT GTA GGT ATC CGC GGT TAC ATG TAC CTG AAA GGT Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly 290 295 300	912
CCG CGT GGT TCT GTT ATG ACT ACC AAC ATC TAC CTG AAC TCT TCC CTG Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu 305 310 315 320	960
TAC CGT GGT ACC AAA TTC ATC ATC AAG AAA TAC GCG TCT GGT AAC AAG Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys 325 330 335	1008
GAC AAT ATC GTT CGC AAC AAT GAT CGT GTA TAC ATC AAT GTT GTA GTT Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val 340 345 350	1056
AAG AAC AAA GAA TAC CGT CTG GCT ACC AAT GCT TCT CAG GCT GGT GTA Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val 355 360 365	1104
GAA AAG ATC TTG TCT GCT CTG GAA ATC CCG GAC GTT GGT AAT CTG TCT Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser 370 375 380	1152
CAG GTA GTT GTA ATG AAA TCC AAG AAC GAC CAG GGT ATC ACT AAC AAA Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys 385 390 395 400	1200
TGC AAA ATG AAT CTG CAG GAC AAC AAT GGT AAC GAT ATC GGT TTC ATC Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile 405 410 415	1248

GGT TTC CAC CAG TTC AAC AAT ATC GCT AAA CTG GTT GCT TCC AAC TGG Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser Asn Trp	1296
420 425 430	

TAC AAT CGT CAG ATC GAA CGT TCC TCT CGC ACT CTG GGT TGC TCT TGG Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp	1344
435 440 445	

GAG TTC ATC CCG GTT GAT GAC GGT TGG GGT GAA CGT CCG CTG Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu	1386
450 455 460	

TAACCCGGGA AAGCTT 1402

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Gly His His His His His His His His Ser Ser Gly His  
1 5 10 15

Ile Glu Gly Arg His Met Ala Ser Met Ala Arg Leu Leu Ser Thr Phe  
20 25 30

Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg  
35 40 45

Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile  
50 55 60

Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile  
65 70 75 80

Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys Asn  
85 90 95

Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp  
100 105 110

Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr  
115 120 125

Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser Leu  
130 135 140

Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys  
145 150 155 160

Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr  
165 170 175

Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn Asn  
180 185 190

Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser  
 195 200 205  
 Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu Asp  
 210 215 220  
 Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu  
 225 230 235 240  
 Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn  
 245 250 255  
 Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln  
 260 265 270  
 Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr  
 275 280 285  
 Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly  
 290 295 300  
 Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu  
 305 310 315 320  
 Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys  
 325 330 335  
 Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val  
 340 345 350  
 Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val  
 355 360 365  
 Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser  
 370 375 380  
 Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys  
 385 390 395 400  
 Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile  
 405 410 415  
 Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser Asn Trp  
 420 425 430  
 Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp  
 435 440 445  
 Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu  
 450 455 460

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3891 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 1..3888

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATG CAA TTT GTT AAT AAA CAA TTT AAT TAT AAA GAT CCT GTA AAT GGT	48
Met Gln Phe Val Asn Lys Gln Phe Asn Tyr Lys Asp Pro Val Asn Gly	
1                      5                     10                     15	
GTT GAT ATT GCT TAT ATA AAA ATT CCA AAT GTA GGA CAA ATG CAA CCA	96
Val Asp Ile Ala Tyr Ile Lys Ile Pro Asn Val Gly Gln Met Gln Pro	
20                    25                    30	
GTA AAA GCT TTT AAA ATT CAT AAT AAA ATA TGG GTT ATT CCA GAA AGA	144
Val Lys Ala Phe Lys Ile His Asn Lys Ile Trp Val Ile Pro Glu Arg	
35                    40                    45	
GAT ACA TTT ACA AAT CCT GAA GAA GGA GAT TTA AAT CCA CCA CCA GAA	192
Asp Thr Phe Thr Asn Pro Glu Glu Gly Asp Leu Asn Pro Pro Pro Glu	
50                    55                    60	
GCA AAA CAA GTT CCA GTT TCA TAT TAT GAT TCA ACA TAT TTA AGT ACA	240
Ala Lys Gln Val Pro Val Ser Tyr Tyr Asp Ser Thr Tyr Leu Ser Thr	
65                    70                    75                    80	
GAT AAT GAA AAA GAT AAT TAT TTA AAG GGA GTT ACA AAA TTA TTT GAG	288
Asp Asn Glu Lys Asp Asn Tyr Leu Lys Gly Val Thr Lys Leu Phe Glu	
85                    90                    95	
AGA ATT TAT TCA ACT GAT CTT GGA AGA ATG TTG TTA ACA TCA ATA GTA	336
Arg Ile Tyr Ser Thr Asp Leu Gly Arg Met Leu Leu Thr Ser Ile Val	
100                  105                  110	
AGG GGA ATA CCA TTT TGG GGT GGA AGT ACA ATA GAT ACA GAA TTA AAA	384
Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys	
115                  120                  125	
GTT ATT GAT ACT AAT TGT ATT AAT GTG ATA CAA CCA GAT GGT AGT TAT	432
Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr	
130                  135                  140	
AGA TCA GAA GAA CTT AAT CTA GTA ATA ATA GGA CCC TCA GCT GAT ATT	480
Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile	
145                  150                  155                  160	
ATA CAG TTT GAA TGT AAA AGC TTT GGA CAT GAA GTT TTG AAT CTT ACG	528
Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr	
165                  170                  175	
CGA AAT GGT TAT GGC TCT ACT CAA TAC ATT AGA TTT AGC CCA GAT TTT	576
Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe	
180                  185                  190	
ACA TTT GGT TTT GAG GAG TCA CTT GAA GTT GAT ACA AAT CCT CTT TTA	624
Thr Phe Gly Phe Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu	
195                  200                  205	
GGT GCA GGC AAA TTT GCT ACA GAT CCA GCA GTA ACA TTA GCA CAT GAA	672
Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu	
210                  215                  220	

CTT ATA CAT GCT GGA CAT AGA TTA TAT GGA ATA GCA ATT AAT CCA AAT Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn 225 230 235 240	720
AGG GTT TTT AAA GTA AAT ACT AAT GCC TAT TAT GAA ATG AGT GGG TTA Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu 245 250 255	768
GAA GTA AGC TTT GAG GAA CTT AGA ACA TTT GGG GGA CAT GAT GCA AAG Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys 260 265 270	816
TTT ATA GAT AGT TTA CAG GAA AAC GAA TTT CGT CTA TAT TAT TAT AAT Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn 275 280 285	864
AAG TTT AAA GAT ATA GCA AGT ACA CTT AAT AAA GCT AAA TCA ATA GTA Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val 290 295 300	912
GGT ACT ACT GCT TCA TTA CAG TAT ATG AAA AAT GTT TTT AAA GAG AAA Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys 305 310 315 320	960
TAT CTC CTA TCT GAA GAT ACA TCT GGA AAA TTT TCG GTA GAT AAA TTA Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu 325 330 335	1008
AAA TTT GAT AAG TTA TAC AAA ATG TTA ACA GAG ATT TAC ACA GAG GAT Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp 340 345 350	1056
AAT TTT GTT AAG TTT TTT AAA GTA CTT AAC AGA AAA ACA TAT TTG AAT Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn 355 360 365	1104
TTT GAT AAA GCC GTA TTT AAG ATA AAT ATA GTA CCT AAG GTA AAT TAC Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr 370 375 380	1152
ACA ATA TAT GAT GGA TTT AAT TTA AGA AAT ACA AAT TTA GCA GCA AAC Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn 385 390 395 400	1200
TTT AAT GGT CAA AAT ACA GAA ATT AAT AAT ATG AAT TTT ACT AAA CTA Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu 405 410 415	1248
AAA AAT TTT ACT GGA TTG TTT GAA TTT TAT AAG TTG CTA TGT GTA AGA Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg 420 425 430	1296
GGG ATA ATA ACT TCT AAA ACT AAA TCA TTA GAT AAA GGA TAC AAT AAG Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Lys Gly Tyr Asn Lys 435 440 445	1344
GCA TTA AAT GAT TTA TGT ATC AAA GTT AAT AAT TGG GAC TTG TTT TTT Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe 450 455 460	1392

AGT CCT TCA GAA GAT AAT TTT ACT AAT GAT CTA AAT AAA GGA GAA GAA		1440
Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu		
465 470 475 480		
ATT ACA TCT GAT ACT AAT ATA GAA GCA GCA GAA GAA AAT ATT AGT TTA		1488
Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu		
485 490 495		
GAT TTA ATA CAA CAA TAT TAT TTA ACC TTT AAT TTT GAT AAT GAA CCT		1536
Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro		
500 505 510		
GAA AAT ATT TCA ATA GAA AAT CTT TCA AGT GAC ATT ATA GGC CAA TTA		1584
Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu		
515 520 525		
GAA CTT ATG CCT AAT ATA GAA AGA TTT CCT AAT GGA AAA AAG TAT GAG		1632
Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu		
530 535 540		
TTA GAT AAA TAT ACT ATG TTC CAT TAT CTT CGT GCT CAA GAA TTT GAA		1680
Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu		
545 550 555 560		
CAT GGT AAA TCT AGG ATT GCT TTA ACA AAT TCT GTT AAC GAA GCA TTA		1728
His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu		
565 570 575		
TTA AAT CCT AGT CGT GTT TAT ACA TTT TTT TCT TCA GAC TAT GTA AAG		1776
Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys		
580 585 590		
AAA GTT AAT AAA GCT ACG GAG GCA GCT ATG TTT TTA GGC TGG GTA GAA		1824
Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu		
595 600 605		
CAA TTA GTA TAT GAT TTT ACC GAT GAA ACT AGC GAA GTA AGT ACT ACG		1872
Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr		
610 615 620		
GAT AAA ATT GCG GAT ATA ACT ATA ATT ATT CCA TAT ATA GGA CCT GCT		1920
Asp Lys Ile Ala Asp Ile Thr Ile Ile Pro Tyr Ile Gly Pro Ala		
625 630 635 640		
TTA AAT ATA GGT AAT ATG TTA TAT AAA GAT GAT TTT GTA GGT GCT TTA		1968
Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu		
645 650 655		
ATA TTT TCA GGA GCT GTT ATT CTG TTA GAA TTT ATA CCA GAG ATT GCA		2016
Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala		
660 665 670		
ATA CCT GTA TTA GGT ACT TTT GCA CTT GTA TCA TAT ATT GCG AAT AAG		2064
Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys		
675 680 685		
GTT CTA ACC GTT CAA ACA ATA GAT AAT GCT TTA AGT AAA AGA AAT GAA		2112
Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu		
690 695 700		

AAA TGG GAT GAG GTC TAT AAA TAT ATA GTA ACA AAT TGG TTA GCA AAG Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys 705 710 715 720	2160
GTT AAT ACA CAG ATT GAT CTA ATA AGA AAA AAA ATG AAA GAA GCT TTA Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu 725 730 735	2208
GAA AAT CAA GCA GAA GCA ACA AAG GCT ATA ATA AAC TAT CAG TAT AAT Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn 740 745 750	2256
CAA TAT ACT GAG GAA GAG AAA AAT AAT ATT AAT TTT AAT ATT GAT GAT Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp 755 760 765	2304
TTA AGT TCG AAA CTT AAT GAG TCT ATA AAT AAA GCT ATG ATT AAT ATA Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile 770 775 780	2352
AAT AAA TTT TTG AAT CAA TGC TCT GTT TCA TAT TTA ATG AAT TCT ATG Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met 785 790 795 800	2400
ATC CCT TAT GGT GTT AAA CGG TTA GAA GAT TTT GAT GCT AGT CTT AAA Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys 805 810 815	2448
GAT GCA TTA TTA AAG TAT ATA TAT GAT AAT AGA GGA ACT TTA ATT GGT Asp Ala Leu Leu Lys Tyr Ile Tyr Asn Arg Gly Thr Leu Ile Gly 820 825 830	2496
CAA GTA GAT AGA TTA AAA GAT AAA GTT AAT AAT ACA CTT AGT ACA GAT Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp 835 840 845	2544
ATA CCT TTT CAG CTT TCC AAA TAC GTA GAT AAT CAA AGA TTA TTA TCT Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser 850 855 860	2592
ACA TTT ACT GAA TAT ATT AAG AAT ATT AAT ACT TCT ATA TTG AAT Thr Phe Thr Glu Tyr Ile Lys Asn Ile Asn Thr Ser Ile Leu Asn 865 870 875 880	2640
TTA AGA TAT GAA AGT AAT CAT TTA ATA GAC TTA TCT AGG TAT GCA TCA Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser 885 890 895	2688
AAA ATA AAT ATT GGT AGT AAA GTA AAT TTT GAT CCA ATA GAT AAA AAT Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn 900 905 910	2736
CAA ATT CAA TTA TTT AAT TTA GAA AGT AGT AAA ATT GAG GTA ATT TTA Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu 915 920 925	2784
AAA AAT GCT ATT GTA TAT AAT AGT ATG TAT GAA AAT TTT AGT ACT AGC Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser 930 935 940	2832

TTT TGG ATA AGA ATT CCT AAG TAT TTT AAC AGT ATA AGT CTA AAT AAT Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn 945 950 955 960	2880
GAA TAT ACA ATA ATA AAT TGT ATG GAA AAT AAT TCA GGA TGG AAA GTA Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val 965 970 975	2928
TCA CTT AAT TAT GGT GAA ATA ATC TGG ACT TTA CAG GAT ACT CAG GAA Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu 980 985 990	2976
ATA AAA CAA AGA GTA GTT TTT AAA TAC AGT CAA ATG ATT AAT ATA TCA Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser 995 1000 1005	3024
GAT TAT ATA AAC AGA TGG ATT TTT GTA ACT ATC ACT AAT AAT AGA TTA Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu 1010 1015 1020	3072
AAT AAC TCT AAA ATT TAT ATA AAT GGA AGA TTA ATA GAT CAA AAA CCA Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro 1025 1030 1035 1040	3120
ATT TCA AAT TTA GGT AAT ATT CAT GCT AGT AAT AAT ATA ATG TTT AAA Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys 1045 1050 1055	3168
TTA GAT GGT TGT AGA GAT ACA CAT AGA TAT ATT TGG ATA AAA TAT TTT Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe 1060 1065 1070	3216
AAT CTT TTT GAT AAG GAA TTA AAT GAA AAA GAA ATC AAA GAT TTA TAT Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr 1075 1080 1085	3264
GAT AAT CAA TCA AAT TCA GGT ATT TTA AAA GAC TTT TGG GGT GAT TAT Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr 1090 1095 1100	3312
TTA CAA TAT GAT AAA CCA TAC TAT ATG TTA AAT TTA TAT GAT CCA AAT Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn 1105 1110 1115 1120	3360
AAA TAT GTC GAT GTA AAT AAT GTA GGT ATT AGA GGT TAT ATG TAT CTT Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu 1125 1130 1135	3408
AAA GGG CCT AGA GGT AGC GTA ATG ACT ACA AAC ATT TAT TTA AAT TCA Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser 1140 1145 1150	3456
AGT TTG TAT AGG GGG ACA AAA TTT ATT ATA AAA AAA TAT GCT TCT GGA Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly 1155 1160 1165	3504
AAT AAA GAT AAT ATT GTT AGA AAT AAT GAT CGT GTA TAT ATT AAT GTA Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val 1170 1175 1180	3552

GTA GTT AAA AAT AAA GAA TAT AGG TTA GCT ACT AAT GCA TCA CAG GCA Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala 1185 1190 1195 1200	3600
GGC GTA GAA AAA ATA CTA AGT GCA TTA GAA ATA CCT GAT GTA GGA AAT Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn 1205 1210 1215	3648
CTA AGT CAA GTA GTA GTA ATG AAG TCA AAA AAT GAT CAA GGA ATA ACA Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr 1220 1225 1230	3696
AAT AAA TGC AAA ATG AAT TTA CAA GAT AAT AAT GGG AAT GAT ATA GGC Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly 1235 1240 1245	3744
TTT ATA GGA TTT CAT CAG TTT AAT AAT ATA GCT AAA CTA GTA GCA AGT Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser 1250 1255 1260	3792
AAT TGG TAT AAT AGA CAA ATA GAA AGA TCT AGT AGG ACT TTG GGT TGC Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys 1265 1270 1275 1280	3840
TCA TGG GAA TTT ATT CCT GTA GAT GAT GGA TGG GGA GAA AGG CCA CTG Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu 1285 1290 1295	3888
TAA	3891

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1296 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Gln	Phe	Val	Asn	Lys	Gln	Phe	Asn	Tyr	Lys	Asp	Pro	Val	Asn	Gly
1				5						10				15	
Val	Asp	Ile	Ala	Tyr	Ile	Lys	Ile	Pro	Asn	Val	Gly	Gln	Met	Gln	Pro
				20						25				30	
Val	Lys	Ala	Phe	Lys	Ile	His	Asn	Lys	Ile	Trp	Val	Ile	Pro	Glu	Arg
				35				40					45		
Asp	Thr	Phe	Thr	Asn	Pro	Glu	Glu	Gly	Asp	Leu	Asn	Pro	Pro	Pro	Glu
					50		55					60			
Ala	Lys	Gln	Val	Pro	Val	Ser	Tyr	Tyr	Asp	Ser	Thr	Tyr	Leu	Ser	Thr
					65		70			75				80	
Asp	Asn	Glu	Lys	Asp	Asn	Tyr	Leu	Lys	Gly	Val	Thr	Lys	Leu	Phe	Glu
					85				90					95	
Arg	Ile	Tyr	Ser	Thr	Asp	Leu	Gly	Arg	Met	Leu	Leu	Thr	Ser	Ile	Val
					100				105				110		

Arg Gly Ile Pro Phe Trp Gly Gly Ser Thr Ile Asp Thr Glu Leu Lys  
115 120 125

Val Ile Asp Thr Asn Cys Ile Asn Val Ile Gln Pro Asp Gly Ser Tyr  
130 135 140

Arg Ser Glu Glu Leu Asn Leu Val Ile Ile Gly Pro Ser Ala Asp Ile  
145 150 155 160

Ile Gln Phe Glu Cys Lys Ser Phe Gly His Glu Val Leu Asn Leu Thr  
165 170 175

Arg Asn Gly Tyr Gly Ser Thr Gln Tyr Ile Arg Phe Ser Pro Asp Phe  
180 185 190

Thr Phe Gly Phe Glu Glu Ser Leu Glu Val Asp Thr Asn Pro Leu Leu  
195 200 205

Gly Ala Gly Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu  
210 215 220

Leu Ile His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn  
225 230 235 240

Arg Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu  
245 250 255

Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala Lys  
260 265 270

Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr Tyr Asn  
275 280 285

Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys Ser Ile Val  
290 295 300

Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val Phe Lys Glu Lys  
305 310 315 320

Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe Ser Val Asp Lys Leu  
325 330 335

Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr Glu Ile Tyr Thr Glu Asp  
340 345 350

Asn Phe Val Lys Phe Phe Lys Val Leu Asn Arg Lys Thr Tyr Leu Asn  
355 360 365

Phe Asp Lys Ala Val Phe Lys Ile Asn Ile Val Pro Lys Val Asn Tyr  
370 375 380

Thr Ile Tyr Asp Gly Phe Asn Leu Arg Asn Thr Asn Leu Ala Ala Asn  
385 390 395 400

Phe Asn Gly Gln Asn Thr Glu Ile Asn Asn Met Asn Phe Thr Lys Leu  
405 410 415

Lys Asn Phe Thr Gly Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg  
420 425 430

Gly Ile Ile Thr Ser Lys Thr Lys Ser Leu Asp Lys Gly Tyr Asn Lys  
435 440 445

Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe  
450 455 460

Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu  
465 470 475 480

Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu  
485 490 495

Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu Pro  
500 505 510

Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln Leu  
515 520 525

Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr Glu  
530 535 540

Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe Glu  
545 550 555 560

His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala Leu  
565 570 575

Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val Lys  
580 585 590

Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val Glu  
595 600 605

Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr Thr  
610 615 620

Asp Lys Ile Ala Asp Ile Thr Ile Ile Pro Tyr Ile Gly Pro Ala  
625 630 635 640

Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu  
645 650 655

Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala  
660 665 670

Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys  
675 680 685

Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu  
690 695 700

Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys  
705 710 715 720

Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu  
725 730 735

Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr Asn  
740 745 750

Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp Asp  
755 760 765

Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn Ile  
770 775 780

Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser Met  
 785 790 795 800  
 Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu Lys  
 805 810 815  
 Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn Arg Gly Thr Leu Ile Gly  
 820 825 830  
 Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr Asp  
 835 840 845  
 Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln Arg Leu Leu Ser  
 850 855 860  
 Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn  
 865 870 875 880  
 Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser  
 885 890 895  
 Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn  
 900 905 910  
 Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu  
 915 920 925  
 Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser  
 930 935 940  
 Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn  
 945 950 955 960  
 Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val  
 965 970 975  
 Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu  
 980 985 990  
 Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser  
 995 1000 1005  
 Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu  
 1010 1015 1020  
 Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro  
 1025 1030 1035 1040  
 Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys  
 1045 1050 1055  
 Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe  
 1060 1065 1070  
 Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr  
 1075 1080 1085  
 Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr  
 1090 1095 1100  
 Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn  
 1105 1110 1115 1120

Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu  
 1125 1130 1135  
 Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser  
 1140 1145 1150  
 Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly  
 1155 1160 1165  
 Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val  
 1170 1175 1180  
 Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala  
 1185 1190 1195 1200  
 Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn  
 1205 1210 1215  
 Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr  
 1220 1225 1230  
 Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly  
 1235 1240 1245  
 Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser  
 1250 1255 1260  
 Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys  
 1265 1270 1275 1280  
 Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu  
 1285 1290 1295

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CGCCATGGCT AGATTATTAT CTACATTAC

30

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCAAGCTTCT TGACAGACTC ATGTAG

26

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGATCTCGAT CCCGCATAAT TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA	60
TTCCCTCTA GAAATAATT TGTTAACCT TAAGAAGGAG ATATACCATG GGCCATCATC	120
ATCATCATCA TCATCATCAT CACAGCAGCG GCCATATCGA AGGTCGTAT ATGGCTAGCA	180
TGGCTAGATT ATTATCTACA TTTACTGAAT ATATTAAGAA TATTATTAAT ACTTCTATAT	240
TGAATTAAAG ATATGAAAGT AATCATTAA TAGACTTATC TAGGTATGCA TCAAAAATAA	300
ATATTGGTAG TAAAGTAAAT TTTGATCAA TAGATAAAAA TCAAATTCAA TTATTTAATT	360
TAGAAAGTAG TAAAATTGAG GTAATTTAA AAAATGCTAT TGTATATAAT AGTATGTATG	420
AAAATTTAG TACTAGCTT TGGATAAGAA TTCCTAAGTA TTTAACAGT ATAAGTCTAA	480
ATAATGAATA TACAATAATA AATTGTATGG AAAATAATC AGGATGGAAA GTATCACTTA	540
ATTATGGTGA AATAATCTGG ACTTTACAGG ATACTCAGGA AATAAAACAA AGAGTAGTTT	600
TTAAATACAG TCAAATGATT AATATATCAG ATTATATAAA CAGATGGATT TTTGTAACCA	660
TCACTAATAA TAGATTAAAT AACTCTAAAA TTTATATAAA TGGAAGATTA ATAGATCAA	720
AACCAATTTC AAATTTAGGT AATATTCTG CTAGTAATAA TATAATGTTT AAATTAGATG	780
GTTGTAGAGA TACACATAGA TATATTTGGA TAAAATATTT TAATCTTTT GATAAGGAAT	840
TAAATGAAAA AGAAATCAA GATTTATATG ATAATCAATC AAATTCAGGT ATTTAAAAG	900
ACTTTGCCCC TGATTATTT CAATATGATA AACCCATACTA TATGTTAAAT TTATATGATC	960
CAAATAATA TGTCGATGTA AATAATGTAG GTATTAGAGG TTATATGTAT CTTAAAGGGC	1020
CTAGAGGTAG CGTAATGACT ACAAACATTT ATTTAAATC AAGTTGTAT AGGGGGACAA	1080
AATTTATTAT AAAAAATAT GCTTCTGGAA ATAAAGATAA TATTGTTAGA AATAATGATC	1140
GTGTATATAT TAATGTAGTA GTAAAAATA AAGAATATAG GTTAGCTACT AATGCATCAC	1200
AGGCAGGCCT AGAAAAATA CTAAGTGCAT TAGAAATACC TGATGTAGGA AATCTAAGTC	1260
AAGTAGTAGT AATGAAGTCA AAAATGATC AAGGAATAAC AAATAATGC AAAATGAATT	1320
TACAAGATAA TAATGGGAAT GATATAGGCT TTATAGGATT TCATCAGTTT AATAATATAG	1380
CTAAACTAGT AGCAAGTAAT TGGTATAATA GACAAATAGA AAGATCTAGT AGGACTTTGG	1440

GTTGCTCATG GGAATTTATT CCTGTAGATG ATGGATGGGG AGAAAGGCCA CTGTAATTAA	1500
TCTCAAACTA CATGAGTCTG TCAAGAACGCT TGCGGCCGCA CTCGAG	1546

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met His His His His His Met Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TATGCATCAC CATCACCATC A 21

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CATGTGATGG TGATGGTGAT GCA 23

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1351 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

## (ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 1..1335

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATG CAT CAC CAT CAC CAT CAC ATG GCT CGT CTG CTG TCT ACC TTC ACT	48
Met His His His His His Met Ala Arg Leu Leu Ser Thr Phe Thr	
1 5 10 15	
GAA TAC ATC AAG AAC ATC ATC AAT ACC TCC ATC CTG AAC CTG CGC TAC	96
Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr	
20 25 30	
GAA TCC AAT CAC CTG ATC GAC CTG TCT CGC TAC GCT TCC AAA ATC AAC	144
Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn	
35 40 45	
ATC GGT TCT AAA GTT AAC TTC GAT CCG ATC GAC AAG AAT CAG ATC CAG	192
Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln	
50 55 60	
CTG TTC AAT CTG GAA TCT TCC AAA ATC GAA GTT ATC CTG AAG AAT GCT	240
Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala	
65 70 75 80	
ATC GTA TAC AAC TCT ATG TAC GAA AAC TTC TCC ACC TCC TTC TGG ATC	288
Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile	
85 90 95	
CGT ATC CCG AAA TAC TTC AAC TCC ATC TCT CTG AAC AAT GAA TAC ACC	336
Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr	
100 105 110	
ATC ATC AAC TGC ATG GAA AAC AAT TCT GGT TGG AAA GTA TCT CTG AAC	384
Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn	
115 120 125	
TAC GGT GAA ATC ATC TGG ACT CTG CAG GAC ACT CAG GAA ATC AAA CAG	432
Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln	
130 135 140	
CGT GTT GTA TTC AAA TAC TCT CAG ATG ATC AAC ATC TCT GAC TAC ATC	480
Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile	
145 150 155 160	
AAT CGC TGG ATC TTC GTT ACC ATC ACC AAC AAT CGT CTG AAT AAC TCC	528
Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser	
165 170 175	
AAA ATC TAC ATC AAC GGC CGT CTG ATC GAC CAG AAA CCG ATC TCC AAT	576
Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn	
180 185 190	
CTG GGT AAC ATC CAC GCT TCT AAT AAC ATC ATG TTC AAA CTG GAC GGT	624
Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly	
195 200 205	
TGT CGT GAC ACT CAC CGC TAC ATC TGG ATC AAA TAC TTC AAT CTG TTC	672
Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe	
210 215 220	

GAC AAA GAA CTG AAC GAA AAA GAA ATC AAA GAC CTG TAC GAC AAC CAG Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln 225 230 235 240	720
TCC AAT TCT GGT ATC CTG AAA GAC TTC TGG GGT GAC TAC CTG CAG TAC Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr 245 250 255	768
GAC AAA CCG TAC TAC ATG CTG AAT CTG TAC GAT CCG AAC AAA TAC GTT Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val 260 265 270	816
GAC GTC AAC AAT GTA GGT ATC CGC GGT TAC ATG TAC CTG AAA GGT CCG Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro 275 280 285	864
CGT GGT TCT GTT ATG ACT ACC AAC ATC TAC CTG AAC TCT TCC CTG TAC Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr 290 295 300	912
CGT GGT ACC AAA TTC ATC ATC AAG AAA TAC GCG TCT GGT AAC AAG GAC Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp 305 310 315 320	960
AAT ATC GTT CGC AAC AAT GAT CGT GTA TAC ATC AAT GTT GTA GTT AAG Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Lys 325 330 335	1008
AAC AAA GAA TAC CGT CTG GCT ACC AAT GCT TCT CAG GCT GGT GTA GAA Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu 340 345 350	1056
AAG ATC TTG TCT GCT CTG GAA ATC CCG GAC GTT GGT AAT CTG TCT CAG Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln 355 360 365	1104
GTA GTT GTA ATG AAA TCC AAG AAC GAC CAG GGT ATC ACT AAC AAA TGC Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys 370 375 380	1152
AAA ATG AAT CTG CAG GAC AAC AAT GGT AAC GAT ATC GGT TTC ATC GGT Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly 385 390 395 400	1200
TTC CAC CAG TTC AAC AAT ATC GCT AAA CTG GTT GCT TCC AAC TGG TAC Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr 405 410 415	1248
AAT CGT CAG ATC GAA CGT TCC TCT CGC ACT CTG GGT TGC TCT TGG GAG Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu 420 425 430	1296
TTC ATC CCG GTT GAT GAC GGT TGG GGT GAA CGT CCG CTG TAACCCGGGA Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu 435 440 445	1345
<b>AAGCTT</b>	<b>1351</b>

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met His His His His His Met Ala Arg Leu Leu Ser Thr Phe Thr  
1 5 10 15

Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr  
20 25 30

Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn  
35 40 45

Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln  
50 55 60

Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala  
65 70 75 80

Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile  
85 90 95

Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr  
100 105 110

Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn  
115 120 125

Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln  
130 135 140

Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile  
145 150 155 160

Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser  
165 170 175

Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn  
180 185 190

Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly  
195 200 205

Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe  
210 215 220

Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln  
225 230 235 240

Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr  
245 250 255

Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val  
260 265 270

Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro  
 275 280 285  
 Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr  
 290 295 300  
 Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp  
 305 310 315 320  
 Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys  
 325 330 335  
 Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu  
 340 345 350  
 Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln  
 355 360 365  
 Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys  
 370 375 380  
 Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly  
 385 390 395 400  
 Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr  
 405 410 415  
 Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu  
 420 425 430  
 Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg Pro Leu  
 435 440 445

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CGCATATGAA TATTCGTCCA TTGCATG

27

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGAAGCTTGC AGGGCAATTAA CATCATG

27

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3876 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..3873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATG CCA GTT ACA ATA AAT AAT TTT AAT TAT AAT GAT CCT ATT GAT AAT Met Pro Val Thr Ile Asn Asn Phe Asn Tyr Asn Asp Pro Ile Asp Asn	48
1 5 10 15	
GAC AAT ATT ATT ATG ATG GAA CCT CCA TTT GCA AGG GGT ACG GGG AGA Asp Asn Ile Ile Met Met Glu Pro Pro Phe Ala Arg Gly Thr Gly Arg	96
20 25 30	
TAT TAT AAA GCT TTT AAA ATC ACA GAT CGT ATT TGG ATA ATA CCC GAA Tyr Tyr Lys Ala Phe Lys Ile Thr Asp Arg Ile Trp Ile Ile Pro Glu	144
35 40 45	
AGA TAT ACT TTT GGA TAT AAA CCT GAG GAT TTT AAT AAA AGT TCC GGT Arg Tyr Thr Phe Gly Tyr Lys Pro Glu Asp Phe Asn Lys Ser Ser Gly	192
50 55 60	
ATT TTT AAT AGA GAT GTT TGT GAA TAT TAT GAT CCA GAT TAC TTA AAT Ile Phe Asn Arg Asp Val Cys Glu Tyr Tyr Asp Pro Asp Tyr Leu Asn	240
65 70 75 80	
ACC AAT GAT AAA AAG AAT ATA TTT TTC CAA ACA TTG ATC AAG TTA TTT Thr Asn Asp Lys Lys Asn Ile Phe Phe Gln Thr Leu Ile Lys Leu Phe	288
85 90 95	
AAT AGA ATC AAA TCA AAA CCA TTG GGT GAA AAG TTA TTA GAG ATG ATT Asn Arg Ile Lys Ser Lys Pro Leu Gly Glu Lys Leu Leu Glu Met Ile	336
100 105 110	
ATA AAT GGT ATA CCT TAT CTT GGA GAT AGA CGT GTT CCA CTC GAA GAG Ile Asn Gly Ile Pro Tyr Leu Gly Asp Arg Arg Val Pro Leu Glu Glu	384
115 120 125	
TTT AAC ACA AAC ATT GCT AGT GTA ACT GTT AAT AAA TTA ATT AGT AAT Phe Asn Thr Asn Ile Ala Ser Val Thr Val Asn Lys Leu Ile Ser Asn	432
130 135 140	
CCA GGA GAA GTG GAG CGA AAA AAA GGT ATT TTC GCA AAT TTA ATA ATA Pro Gly Glu Val Glu Arg Lys Lys Gly Ile Phe Ala Asn Leu Ile Ile	480
145 150 155 160	
TTT GGA CCT GGG CCA GTT TTA AAT GAA AAT GAG ACT ATA GAT ATA GGT Phe Gly Pro Gly Pro Val Leu Asn Glu Asn Glu Thr Ile Asp Ile Gly	528
165 170 175	

ATA CAA AAT CAT TTT GCA TCA AGG GAA GGC TTT GGG GGT ATA ATG CAA Ile Gln Asn His Phe Ala Ser Arg Glu Gly Phe Gly Gly Ile Met Gln 180 185 190	576
ATG AAA TTT TGT CCA GAA TAT GTA AGC GTA TTT AAT AAT GTT CAA GAA Met Lys Phe Cys Pro Glu Tyr Val Ser Val Phe Asn Asn Val Gln Glu 195 200 205	624
AAC AAA GGC GCA AGT ATA TTT AAT AGA CGT GGA TAT TTT TCA GAT CCA Asn Lys Gly Ala Ser Ile Phe Asn Arg Arg Gly Tyr Phe Ser Asp Pro 210 215 220	672
GCC TTG ATA TTA ATG CAT GAA CTT ATA CAT GTT TTG CAT GGA TTA TAT Ala Leu Ile Leu Met His Glu Leu Ile His Val Leu His Gly Leu Tyr 225 230 235 240	720
GGC ATT AAA GTA GAT GAT TTA CCA ATT GTA CCA AAT GAA AAA AAA TTT Gly Ile Lys Val Asp Asp Leu Pro Ile Val Pro Asn Glu Lys Lys Phe 245 250 255	768
TTT ATG CAA TCT ACA GAT ACT ATA CAG GCA GAA GAA CTA TAT ACA TTT Phe Met Gln Ser Thr Asp Thr Ile Gln Ala Glu Glu Leu Tyr Thr Phe 260 265 270	816
GGA GGA CAA GAT CCC AGC ATC ATA TCT CCT TCT ACA GAT AAA AGT ATC Gly Gly Gln Asp Pro Ser Ile Ile Ser Pro Ser Thr Asp Lys Ser Ile 275 280 285	864
TAT GAT AAA GTT TTG CAA AAT TTT AGG GGG ATA GTT GAT AGA CTT AAC Tyr Asp Lys Val Leu Gln Asn Phe Arg Gly Ile Val Asp Arg Leu Asn 290 295 300	912
AAG GTT TTA GTT TGC ATA TCA GAT CCT AAC ATT AAC ATT AAT ATA TAT Lys Val Leu Val Cys Ile Ser Asp Pro Asn Ile Asn Ile Asn Ile Tyr 305 310 315 320	960
AAA AAT AAA TTT AAA GAT AAA TAT AAA TTC GTT GAA GAT TCT GAA GGA Lys Asn Lys Phe Lys Asp Lys Tyr Lys Phe Val Glu Asp Ser Glu Gly 325 330 335	1008
AAA TAT AGT ATA GAT GTA GAA AGT TTC AAT AAA TTA TAT AAA AGC TTA Lys Tyr Ser Ile Asp Val Glu Ser Phe Asn Lys Leu Tyr Lys Ser Leu 340 345 350	1056
ATG TTA GGT TTT ACA GAA ATT AAT ATA GCA GAA AAT TAT AAA ATA AAA Met Leu Gly Phe Thr Glu Ile Asn Ile Ala Glu Asn Tyr Lys Ile Lys 355 360 365	1104
ACT AGA GCT TCT TAT TTT AGT GAT TCC TTA CCA CCA GTA AAA ATA AAA Thr Arg Ala Ser Tyr Phe Ser Asp Ser Leu Pro Pro Val Lys Ile Lys 370 375 380	1152
AAT TTA TTA GAT AAT GAA ATC TAT ACT ATA GAG GAA GGG TTT AAT ATA Asn Leu Leu Asp Asn Glu Ile Tyr Thr Ile Glu Glu Gly Phe Asn Ile 385 390 395 400	1200
TCT GAT AAA AAT ATG GGA AAA GAA TAT AGG GGT CAG AAT AAA GCT ATA Ser Asp Lys Asn Met Gly Lys Glu Tyr Arg Gly Gln Asn Lys Ala Ile 405 410 415	1248

AAT AAA CAA GCT TAT GAA GAA ATC AGC AAG GAG CAT TTG GCT GTA TAT Asn Lys Gln Ala Tyr Glu Glu Ile Ser Lys Glu His Leu Ala Val Tyr 420 425 430	1296
AAG ATA CAA ATG TGT AAA AGT GTT AAA GTT CCA GGA ATA TGT ATT GAT Lys Ile Gln Met Cys Lys Ser Val Lys Val Pro Gly Ile Cys Ile Asp 435 440 445	1344
GTC GAT AAT GAA AAT TTG TTC TTT ATA GCT GAT AAA AAT AGT TTT TCA Val Asp Asn Glu Asn Leu Phe Phe Ile Ala Asp Lys Asn Ser Phe Ser 450 455 460	1392
GAT GAT TTA TCT AAA AAT GAA AGA GTA GAA TAT AAT ACA CAG AAT AAT Asp Asp Leu Ser Lys Asn Glu Arg Val Glu Tyr Asn Thr Gln Asn Asn 465 470 475 480	1440
TAT ATA GGA AAT GAC TTT CCT ATA AAT GAA TTA ATT TTA GAT ACT GAT Tyr Ile Gly Asn Asp Phe Pro Ile Asn Glu Leu Ile Leu Asp Thr Asp 485 490 495	1488
TTA ATA AGT AAA ATA GAA TTA CCA AGT GAA AAT ACA GAA TCA CTT ACT Leu Ile Ser Lys Ile Glu Leu Pro Ser Glu Asn Thr Glu Ser Leu Thr 500 505 510	1536
GAT TTT AAT GTA GAT GTT CCA GTA TAT GAA AAA CAA CCC GCT ATA AAA Asp Phe Asn Val Asp Val Pro Val Tyr Glu Lys Gln Pro Ala Ile Lys 515 520 525	1584
AAA GTT TTT ACA GAT GAA AAT ACC ATC TTT CAA TAT TTA TAC TCT CAG Lys Val Phe Thr Asp Glu Asn Thr Ile Phe Gln Tyr Leu Tyr Ser Gln 530 535 540	1632
ACA TTT CCT CTA AAT ATA AGA GAT ATA AGT TTA ACA TCT TCA TTT GAT Thr Phe Pro Leu Asn Ile Arg Asp Ile Ser Leu Thr Ser Ser Phe Asp 545 550 555 560	1680
GAT GCA TTA TTA GTT TCT AGC AAA GTT TAT TCA TTT TTT TCT ATG GAT Asp Ala Leu Leu Val Ser Ser Lys Val Tyr Ser Phe Phe Ser Met Asp 565 570 575	1728
TAT ATT AAA ACT GCT AAT AAA GTA GTA GAA GCA GGA TTA TTT GCA GGT Tyr Ile Lys Thr Ala Asn Lys Val Val Glu Ala Gly Leu Phe Ala Gly 580 585 590	1776
TGG GTG AAA CAG ATA GTA GAT GAT TTT GTA ATC GAA GCT AAT AAA AGC Trp Val Lys Gln Ile Val Asp Asp Phe Val Ile Glu Ala Asn Lys Ser 595 600 605	1824
AGT ACT ATG GAT AAA ATT GCA GAT ATA TCT CTA ATT GTT CCT TAT ATA Ser Thr Met Asp Lys Ile Ala Asp Ile Ser Leu Ile Val Pro Tyr Ile 610 615 620	1872
GGA TTA GCT TTA AAT GTA GGA GAT GAA ACA GCT AAA GGA AAT TTT GAA Gly Leu Ala Leu Asn Val Gly Asp Glu Thr Ala Lys Gly Asn Phe Glu 625 630 635 640	1920
AGT GCT TTT GAG ATT GCA GGA TCC AGT ATT TTA CTA GAA TTT ATA CCA Ser Ala Phe Glu Ile Ala Gly Ser Ser Ile Leu Leu Glu Phe Ile Pro 645 650 655	1968

GAA CTT TTA ATA CCT GTA GTT GGA GTC TTT TTA GAA TCA TAT ATT Glu Leu Leu Ile Pro Val Val Gly Val Phe Leu Leu Glu Ser Tyr Ile 660 665 670	2016
GAC AAT AAA AAT AAA ATT ATT AAA ACA ATA GAT AAT GCT TTA ACT AAA Asp Asn Lys Asn Lys Ile Ile Lys Thr Ile Asp Asn Ala Leu Thr Lys 675 680 685	2064
AGA GTG GAA AAA TGG ATT GAT ATG TAC GGA TTA ATA GTA GCG CAA TGG Arg Val Glu Lys Trp Ile Asp Met Tyr Gly Leu Ile Val Ala Gln Trp 690 695 700	2112
CTC TCA ACA GTT AAT ACT CAA TTT TAT ACA ATA AAA GAG GGA ATG TAT Leu Ser Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Gly Met Tyr 705 710 715 720	2160
AAG GCT TTA AAT TAT CAA GCA CAA GCA TTG GAA GAA ATA ATA AAA TAC Lys Ala Leu Asn Tyr Gln Ala Gln Ala Leu Glu Glu Ile Ile Lys Tyr 725 730 735	2208
AAA TAT AAT ATA TAT TCT GAA GAG GAA AAG TCA AAT ATT AAC ATC AAT Lys Tyr Asn Ile Tyr Ser Glu Glu Lys Ser Asn Ile Asn Ile Asn 740 745 750	2256
TTT AAT GAT ATA AAT TCT AAA CTT AAT GAT GGT ATT AAC CAA GCT ATG Phe Asn Asp Ile Asn Ser Lys Leu Asn Asp Gly Ile Asn Gln Ala Met 755 760 765	2304
GAT AAT ATA AAT GAT TTT ATA AAT GAA TGT TCT GTA TCA TAT TTA ATG Asp Asn Ile Asn Asp Phe Ile Asn Glu Cys Ser Val Ser Tyr Leu Met 770 775 780	2352
AAA AAA ATG ATT CCA TTA GCT GTA AAA AAA TTA CTA GAC TTT GAT AAT Lys Lys Met Ile Pro Leu Ala Val Lys Lys Leu Leu Asp Phe Asp Asn 785 790 795 800	2400
ACT CTC AAA AAA AAT TTA TTA AAT TAT ATA GAT GAA AAT AAA TTA TAT Thr Leu Lys Lys Asn Leu Leu Asn Tyr Ile Asp Glu Asn Lys Leu Tyr 805 810 815	2448
TTA ATT GGA AGT GTA GAA GAT GAA AAA TCA AAA GTA GAT AAA TAC TTG Leu Ile Gly Ser Val Glu Asp Glu Lys Ser Lys Val Asp Lys Tyr Leu 820 825 830	2496
AAA ACC ATT ATA CCA TTT GAT CTT TCA ACG TAT TCT AAT ATT GAA ATA Lys Thr Ile Ile Pro Phe Asp Leu Ser Thr Tyr Ser Asn Ile Glu Ile 835 840 845	2544
CTA ATA AAA ATA TTT AAT AAA TAT AAT AGC GAA ATT TTA AAT ATT ATT Leu Ile Lys Ile Phe Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile 850 855 860	2592
ATC TTA AAT TTA AGA TAT AGA GAT AAT ATT TTA ATA GAT TTA TCA GGA Ile Leu Asn Leu Arg Tyr Arg Asp Asn Asn Leu Ile Asp Leu Ser Gly 865 870 875 880	2640
TAT GGA GCA AAG GTA GAG GTA TAT GAT GGG GTC AAG CTT AAT GAT AAA Tyr Gly Ala Lys Val Glu Val Tyr Asp Gly Val Lys Leu Asn Asp Lys 885 890 895	2688

AAT CAA TTT AAA TTA ACT AGT TCA GCA GAT AGT AAG ATT AGA GTC ACT Asn Gln Phe Lys Leu Thr Ser Ser Ala Asp Ser Lys Ile Arg Val Thr 900 905 910	2736
CAA AAT CAG AAT ATT ATA TTT AAT AGT ATG TTC CTT GAT TTT AGC GTT Gln Asn Gln Asn Ile Ile Phe Asn Ser Met Phe Leu Asp Phe Ser Val 915 920 925	2784
AGC TTT TGG ATA AGG ATA CCT AAA TAT AGG AAT GAT GAT ATA CAA AAT Ser Phe Trp Ile Arg Ile Pro Lys Tyr Arg Asn Asp Asp Ile Gln Asn 930 935 940	2832
TAT ATT CAT AAT GAA TAT ACG ATA ATT AAT TGT ATG AAA AAT AAT TCA Tyr Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser 945 950 955 960	2880
GGC TGG AAA ATA TCT ATT AGG GGT AAT AGG ATA ATA TGG ACC TTA ATT Gly Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile 965 970 975	2928
GAT ATA AAT GGA AAA ACC AAA TCA GTA TTT TTT GAA TAT AAC ATA AGA Asp Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg 980 985 990	2976
GAA GAT ATA TCA GAG TAT ATA AAT AGA TGG TTT TTT GTA ACT ATT ACT Glu Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr 995 1000 1005	3024
AAT AAT TTG GAT AAT GCT AAA ATT TAT ATT AAT GGC ACG TTA GAA TCA Asn Asn Leu Asp Asn Ala Lys Ile Tyr Ile Asn Gly Thr Leu Glu Ser 1010 1015 1020	3072
AAT ATG GAT ATT AAA GAT ATA GGA GAA GTT ATT GTT AAT GGT GAA ATA Asn Met Asp Ile Lys Asp Ile Gly Glu Val Ile Val Asn Gly Glu Ile 1025 1030 1035 1040	3120
ACA TTT AAA TTA GAT GGT GAT GTA GAT AGA ACA CAA TTT ATT TGG ATG Thr Phe Lys Leu Asp Gly Asp Val Asp Arg Thr Gln Phe Ile Trp Met 1045 1050 1055	3168
AAA TAT TTT AGT ATT TTT AAT ACG CAA TTA AAT CAA TCA AAT ATT AAA Lys Tyr Phe Ser Ile Phe Asn Thr Gln Leu Asn Gln Ser Asn Ile Lys 1060 1065 1070	3216
GAG ATA TAT AAA ATT CAA TCA TAT AGC GAA TAC TTA AAA GAT TTT TGG Glu Ile Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp 1075 1080 1085	3264
GGA AAT CCT TTA ATG TAT AAT AAA GAA TAT TAT ATG TTT AAT GCG GGG Gly Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly 1090 1095 1100	3312
AAT AAA AAT TCA TAT ATT AAA CTA GTG AAA GAT TCA TCT GTA GGT GAA Asn Lys Asn Ser Tyr Ile Lys Leu Val Lys Asp Ser Ser Val Gly Glu 1105 1110 1115 1120	3360
ATA TTA ATA CGT AGC AAA TAT AAT CAG AAT TCC AAT TAT ATA AAT TAT Ile Leu Ile Arg Ser Lys Tyr Asn Gln Asn Ser Asn Tyr Ile Asn Tyr 1125 1130 1135	3408

AGA AAT TTA TAT ATT GGA GAA AAA TTT ATT ATA AGA AGA GAG TCA AAT Arg Asn Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Glu Ser Asn 1140 1145 1150	3456
TCT CAA TCT ATA AAT GAT GAT ATA GTT AGA AAA GAA GAT TAT ATA CAT Ser Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile His 1155 1160 1165	3504
CTA GAT TTG GTA CTT CAC CAT GAA GAG TGG AGA GTA TAT GCC TAT AAA Leu Asp Leu Val Leu His His Glu Glu Trp Arg Val Tyr Ala Tyr Lys 1170 1175 1180	3552
TAT TTT AAG GAA CAG GAA GAA AAA TTG TTT TTA TCT ATT ATA AGT GAT Tyr Phe Lys Glu Gln Glu Glu Lys Leu Phe Leu Ser Ile Ile Ser Asp 1185 1190 1195 1200	3600
TCT AAT GAA TTT TAT AAG ACT ATA GAA ATA AAA GAA TAT GAT GAA CAG Ser Asn Glu Phe Tyr Lys Thr Ile Glu Ile Lys Glu Tyr Asp Glu Gln 1205 1210 1215	3648
CCA TCA TAT AGT TGT CAG TTG CTT TTT AAA AAA GAT GAA GAA AGT ACT Pro Ser Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr 1220 1225 1230	3696
GAT GAT ATA GGA TTG ATT GGT ATT CAT CGT TTC TAC GAA TCT GGA GTT Asp Asp Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Val 1235 1240 1245	3744
TTA CGT AAA AAG TAT AAA GAT TAT TTT TGT ATA AGT AAA TGG TAC TTA Leu Arg Lys Lys Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu 1250 1255 1260	3792
AAA GAG GTA AAA AGG AAA CCA TAT AAG TCA AAT TTG GGA TGT AAT TGG Lys Glu Val Lys Arg Lys Pro Tyr Lys Ser Asn Leu Gly Cys Asn Trp 1265 1270 1275 1280	3840
CAG TTT ATT CCT AAA GAT GAA GGG TGG ACT GAA TAA Gln Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu 1285 1290	3876

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1291 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Pro Val Thr Ile Asn Asn Phe Asn Tyr Asn Asp Pro Ile Asp Asn 1 5 10 15
Asp Asn Ile Ile Met Met Glu Pro Pro Phe Ala Arg Gly Thr Gly Arg 20 25 30
Tyr Tyr Lys Ala Phe Lys Ile Thr Asp Arg Ile Trp Ile Ile Pro Glu 35 40 45
Arg Tyr Thr Phe Gly Tyr Lys Pro Glu Asp Phe Asn Lys Ser Ser Gly 50 55 60

Ile Phe Asn Arg Asp Val Cys Glu Tyr Tyr Asp Pro Asp Tyr Leu Asn  
 65 70 75 80  
 Thr Asn Asp Lys Lys Asn Ile Phe Phe Gln Thr Leu Ile Lys Leu Phe  
 85 90 95  
 Asn Arg Ile Lys Ser Lys Pro Leu Gly Glu Lys Leu Leu Glu Met Ile  
 100 105 110  
 Ile Asn Gly Ile Pro Tyr Leu Gly Asp Arg Arg Val Pro Leu Glu Glu  
 115 120 125  
 Phe Asn Thr Asn Ile Ala Ser Val Thr Val Asn Lys Leu Ile Ser Asn  
 130 135 140  
 Pro Gly Glu Val Glu Arg Lys Lys Gly Ile Phe Ala Asn Leu Ile Ile  
 145 150 155 160  
 Phe Gly Pro Gly Pro Val Leu Asn Glu Asn Glu Thr Ile Asp Ile Gly  
 165 170 175  
 Ile Gln Asn His Phe Ala Ser Arg Glu Gly Phe Gly Gly Ile Met Gln  
 180 185 190  
 Met Lys Phe Cys Pro Glu Tyr Val Ser Val Phe Asn Asn Val Gln Glu  
 195 200 205  
 Asn Lys Gly Ala Ser Ile Phe Asn Arg Arg Gly Tyr Phe Ser Asp Pro  
 210 215 220  
 Ala Leu Ile Leu Met His Glu Leu Ile His Val Leu His Gly Leu Tyr  
 225 230 235 240  
 Gly Ile Lys Val Asp Asp Leu Pro Ile Val Pro Asn Glu Lys Lys Phe  
 245 250 255  
 Phe Met Gln Ser Thr Asp Thr Ile Gln Ala Glu Glu Leu Tyr Thr Phe  
 260 265 270  
 Gly Gly Gln Asp Pro Ser Ile Ile Ser Pro Ser Thr Asp Lys Ser Ile  
 275 280 285  
 Tyr Asp Lys Val Leu Gln Asn Phe Arg Gly Ile Val Asp Arg Leu Asn  
 290 295 300  
 Lys Val Leu Val Cys Ile Ser Asp Pro Asn Ile Asn Ile Asn Ile Tyr  
 305 310 315 320  
 Lys Asn Lys Phe Lys Asp Lys Tyr Lys Phe Val Glu Asp Ser Glu Gly  
 325 330 335  
 Lys Tyr Ser Ile Asp Val Glu Ser Phe Asn Lys Leu Tyr Lys Ser Leu  
 340 345 350  
 Met Leu Gly Phe Thr Glu Ile Asn Ile Ala Glu Asn Tyr Lys Ile Lys  
 355 360 365  
 Thr Arg Ala Ser Tyr Phe Ser Asp Ser Leu Pro Pro Val Lys Ile Lys  
 370 375 380  
 Asn Leu Leu Asp Asn Glu Ile Tyr Thr Ile Glu Glu Gly Phe Asn Ile  
 385 390 395 400

Ser Asp Lys Asn Met Gly Lys Glu Tyr Arg Gly Gln Asn Lys Ala Ile  
405 410 415

Asn Lys Gln Ala Tyr Glu Glu Ile Ser Lys Glu His Leu Ala Val Tyr  
420 425 430

Lys Ile Gln Met Cys Lys Ser Val Lys Val Pro Gly Ile Cys Ile Asp  
435 440 445

Val Asp Asn Glu Asn Leu Phe Phe Ile Ala Asp Lys Asn Ser Phe Ser  
450 455 460

Asp Asp Leu Ser Lys Asn Glu Arg Val Glu Tyr Asn Thr Gln Asn Asn  
465 470 475 480

Tyr Ile Gly Asn Asp Phe Pro Ile Asn Glu Leu Ile Leu Asp Thr Asp  
485 490 495

Leu Ile Ser Lys Ile Glu Leu Pro Ser Glu Asn Thr Glu Ser Leu Thr  
500 505 510

Asp Phe Asn Val Asp Val Pro Val Tyr Glu Lys Gln Pro Ala Ile Lys  
515 520 525

Lys Val Phe Thr Asp Glu Asn Thr Ile Phe Gln Tyr Leu Tyr Ser Gln  
530 535 540

Thr Phe Pro Leu Asn Ile Arg Asp Ile Ser Leu Thr Ser Ser Phe Asp  
545 550 555 560

Asp Ala Leu Leu Val Ser Ser Lys Val Tyr Ser Phe Phe Ser Met Asp  
565 570 575

Tyr Ile Lys Thr Ala Asn Lys Val Val Glu Ala Gly Leu Phe Ala Gly  
580 585 590

Trp Val Lys Gln Ile Val Asp Asp Phe Val Ile Glu Ala Asn Lys Ser  
595 600 605

Ser Thr Met Asp Lys Ile Ala Asp Ile Ser Leu Ile Val Pro Tyr Ile  
610 615 620

Gly Leu Ala Leu Asn Val Gly Asp Glu Thr Ala Lys Gly Asn Phe Glu  
625 630 635 640

Ser Ala Phe Glu Ile Ala Gly Ser Ser Ile Leu Leu Glu Phe Ile Pro  
645 650 655

Glu Leu Leu Ile Pro Val Val Gly Val Phe Leu Leu Glu Ser Tyr Ile  
660 665 670

Asp Asn Lys Asn Lys Ile Ile Lys Thr Ile Asp Asn Ala Leu Thr Lys  
675 680 685

Arg Val Glu Lys Trp Ile Asp Met Tyr Gly Leu Ile Val Ala Gln Trp  
690 695 700

Leu Ser Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Gly Met Tyr  
705 710 715 720

Lys Ala Leu Asn Tyr Gln Ala Gln Ala Leu Glu Glu Ile Ile Lys Tyr  
725 730 735

Lys Tyr Asn Ile Tyr Ser Glu Glu Glu Lys Ser Asn Ile Asn Ile Asn  
740 745 750

Phe Asn Asp Ile Asn Ser Lys Leu Asn Asp Gly Ile Asn Gln Ala Met  
755 760 765

Asp Asn Ile Asn Asp Phe Ile Asn Glu Cys Ser Val Ser Tyr Leu Met  
770 775 780

Lys Lys Met Ile Pro Leu Ala Val Lys Lys Leu Leu Asp Phe Asp Asn  
785 790 795 800

Thr Leu Lys Lys Asn Leu Leu Asn Tyr Ile Asp Glu Asn Lys Leu Tyr  
805 810 815

Leu Ile Gly Ser Val Glu Asp Glu Lys Ser Lys Val Asp Lys Tyr Leu  
820 825 830

Lys Thr Ile Ile Pro Phe Asp Leu Ser Thr Tyr Ser Asn Ile Glu Ile  
835 840 845

Leu Ile Lys Ile Phe Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile  
850 855 860

Ile Leu Asn Leu Arg Tyr Arg Asp Asn Asn Leu Ile Asp Leu Ser Gly  
865 870 875 880

Tyr Gly Ala Lys Val Glu Val Tyr Asp Gly Val Lys Leu Asn Asp Lys  
885 890 895

Asn Gln Phe Lys Leu Thr Ser Ser Ala Asp Ser Lys Ile Arg Val Thr  
900 905 910

Gln Asn Gln Asn Ile Ile Phe Asn Ser Met Phe Leu Asp Phe Ser Val  
915 920 925

Ser Phe Trp Ile Arg Ile Pro Lys Tyr Arg Asn Asp Asp Ile Gln Asn  
930 935 940

Tyr Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser  
945 950 955 960

Gly Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile  
965 970 975

Asp Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg  
980 985 990

Glu Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr  
995 1000 1005

Asn Asn Leu Asp Asn Ala Lys Ile Tyr Ile Asn Gly Thr Leu Glu Ser  
1010 1015 1020

Asn Met Asp Ile Lys Asp Ile Gly Glu Val Ile Val Asn Gly Glu Ile  
1025 1030 1035 1040

Thr Phe Lys Leu Asp Gly Asp Val Asp Arg Thr Gln Phe Ile Trp Met  
1045 1050 1055

Lys Tyr Phe Ser Ile Phe Asn Thr Gln Leu Asn Gln Ser Asn Ile Lys  
1060 1065 1070

Glu Ile Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp  
 1075 1080 1085  
 Gly Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly  
 1090 1095 1100  
 Asn Lys Asn Ser Tyr Ile Lys Leu Val Lys Asp Ser Ser Val Gly Glu  
 1105 1110 1115 1120  
 Ile Leu Ile Arg Ser Lys Tyr Asn Gln Asn Ser Asn Tyr Ile Asn Tyr  
 1125 1130 1135  
 Arg Asn Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Glu Ser Asn  
 1140 1145 1150  
 Ser Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile His  
 1155 1160 1165  
 Leu Asp Leu Val Leu His His Glu Glu Trp Arg Val Tyr Ala Tyr Lys  
 1170 1175 1180  
 Tyr Phe Lys Glu Gln Glu Glu Lys Leu Phe Leu Ser Ile Ile Ser Asp  
 1185 1190 1195 1200  
 Ser Asn Glu Phe Tyr Lys Thr Ile Glu Ile Lys Glu Tyr Asp Glu Gln  
 1205 1210 1215  
 Pro Ser Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr  
 1220 1225 1230  
 Asp Asp Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Val  
 1235 1240 1245  
 Leu Arg Lys Lys Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu  
 1250 1255 1260  
 Lys Glu Val Lys Arg Lys Pro Tyr Lys Ser Asn Leu Gly Cys Asn Trp  
 1265 1270 1275 1280  
 Gln Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu  
 1285 1290

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3876 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..3873
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATG CCA ACA ATA AAT AAT TTT AAT TAT AAT GAT CCT ATT GAT AAT  
 Met Pro Val Thr Ile Asn Asn Phe Asn Tyr Asn Asp Pro Ile Asp Asn  
 1 5 10 15

AAT AAT ATT ATT ATG ATG GAG CCT CCA TTT GCG AGA GGT ACG GGG AGA Asn Asn Ile Ile Met Met Glu Pro Pro Phe Ala Arg Gly Thr Gly Arg 20 25 30	96
TAT TAT AAA GCT TTT AAA ATC ACA GAT CGT ATT TGG ATA ATA CCG GAA Tyr Tyr Lys Ala Phe Lys Ile Thr Asp Arg Ile Trp Ile Ile Pro Glu 35 40 45	144
AGA TAT ACT TTT GGA TAT AAA CCT GAG GAT TTT AAT AAA AGT TCC GGT Arg Tyr Thr Phe Gly Tyr Lys Pro Glu Asp Phe Asn Lys Ser Ser Gly 50 55 60	192
ATT TTT AAT AGA GAT GTT TGT GAA TAT TAT GAT CCA GAT TAC TTA AAT Ile Phe Asn Arg Asp Val Cys Glu Tyr Tyr Asp Pro Asp Tyr Leu Asn 65 70 75 80	240
ACT AAT GAT AAA AAG AAT ATA TTT TTA CAA ACA ATG ATC AAG TTA TTT Thr Asn Asp Lys Lys Asn Ile Phe Leu Gln Thr Met Ile Lys Leu Phe 85 90 95	288
AAT AGA ATC AAA TCA AAA CCA TTG GGT GAA AAG TTA TTA GAG ATG ATT Asn Arg Ile Lys Ser Lys Pro Leu Gly Glu Lys Leu Leu Glu Met Ile 100 105 110	336
ATA AAT GGT ATA CCT TAT CTT GGA GAT AGA CGT GTT CCA CTC GAA GAG Ile Asn Gly Ile Pro Tyr Leu Gly Asp Arg Arg Val Pro Leu Glu Glu 115 120 125	384
TTT AAC ACA AAC ATT GCT AGT GTA ACT GTT AAT AAA TTA ATC AGT AAT Phe Asn Thr Asn Ile Ala Ser Val Thr Val Asn Lys Leu Ile Ser Asn 130 135 140	432
CCA GGA GAA GTG GAG CGA AAA AAA GGT ATT TTC GCA AAT TTA ATA ATA Pro Gly Glu Val Glu Arg Lys Lys Gly Ile Phe Ala Asn Leu Ile Ile 145 150 155 160	480
TTT GGA CCT GGG CCA GTT TTA AAT GAA AAT GAG ACT ATA GAT ATA GGT Phe Gly Pro Gly Pro Val Leu Asn Glu Asn Glu Thr Ile Asp Ile Gly 165 170 175	528
ATA CAA AAT CAT TTT GCA TCA AGG GAA GGC TTC GGG GGT ATA ATG CAA Ile Gln Asn His Phe Ala Ser Arg Glu Gly Phe Gly Gly Ile Met Gln 180 185 190	576
ATG AAG TTT TGC CCA GAA TAT GTA AGC GTA TTT AAT AAT GTT CAA GAA Met Lys Phe Cys Pro Glu Tyr Val Ser Val Phe Asn Asn Val Gln Glu 195 200 205	624
AAC AAA GGC GCA AGT ATA TTT AAT AGA CGT GGA TAT TTT TCA GAT CCA Asn Lys Gly Ala Ser Ile Phe Asn Arg Arg Gly Tyr Phe Ser Asp Pro 210 215 220	672
GCC TTG ATA TTA ATG CAT GAA CTT ATA CAT GTT TTA CAT GGA TTA TAT Ala Leu Ile Leu Met His Glu Leu Ile His Val Leu His Gly Leu Tyr 225 230 235 240	720
GGC ATT AAA GTA GAT GAT TTA CCA ATT GTA CCA AAT GAA AAA AAA TTT Gly Ile Lys Val Asp Asp Leu Pro Ile Val Pro Asn Glu Lys Lys Phe 245 250 255	768

TTT ATG CAA TCT ACA GAT GCT ATA CAG GCA GAA GAA CTA TAT ACA TTT Phe Met Gln Ser Thr Asp Ala Ile Gln Ala Glu Glu Leu Tyr Thr Phe 260 265 270	816
GGA GGA CAA GAT CCC AGC ATC ATA ACT CCT TCT ACG GAT AAA AGT ATC Gly Gly Gln Asp Pro Ser Ile Ile Thr Pro Ser Thr Asp Lys Ser Ile 275 280 285	864
TAT GAT AAA GTT TTG CAA AAT TTT AGA GGG ATA GTT GAT AGA CTT AAC Tyr Asp Lys Val Leu Gln Asn Phe Arg Gly Ile Val Asp Arg Leu Asn 290 295 300	912
AAG GTT TTA GTT TGC ATA TCA GAT CCT AAC ATT AAT ATT AAT ATA TAT Lys Val Leu Val Cys Ile Ser Asp Pro Asn Ile Asn Ile Asn Ile Tyr 305 310 315 320	960
AAA AAT AAA TTT AAA GAT AAA TAT AAA TTC GTT GAA GAT TCT GAG GGA Lys Asn Lys Phe Lys Asp Lys Tyr Lys Phe Val Glu Asp Ser Glu Gly 325 330 335	1008
AAA TAT AGT ATA GAT GTA GAA AGT TTT GAT AAA TTA TAT AAA AGC TTA Lys Tyr Ser Ile Asp Val Glu Ser Phe Asp Lys Leu Tyr Lys Ser Leu 340 345 350	1056
ATG TTT GGT TTT ACA GAA ACT AAT ATA GCA GAA AAT TAT AAA ATA AAA Met Phe Gly Phe Thr Glu Thr Asn Ile Ala Glu Asn Tyr Lys Ile Lys 355 360 365	1104
ACT AGA GCT TCT TAT TTT AGT GAT TCC TTA CCA CCA GTA AAA ATA AAA Thr Arg Ala Ser Tyr Phe Ser Asp Ser Leu Pro Pro Val Lys Ile Lys 370 375 380	1152
AAT TTA TTA GAT AAT GAA ATC TAT ACT ATA GAG GAA GGG TTT AAT ATA Asn Leu Leu Asp Asn Glu Ile Tyr Thr Ile Glu Glu Gly Phe Asn Ile 385 390 395 400	1200
TCT GAT AAA GAT ATG GAA AAA GAA TAT AGA GGT CAG AAT AAA GCT ATA Ser Asp Lys Asp Met Glu Lys Glu Tyr Arg Gly Gln Asn Lys Ala Ile 405 410 415	1248
AAT AAA CAA GCT TAT GAA GAA ATT AGC AAG GAG CAT TTG GCT GTA TAT Asn Lys Gln Ala Tyr Glu Glu Ile Ser Lys Glu His Leu Ala Val Tyr 420 425 430	1296
AAG ATA CAA ATG TGT AAA AGT GTT AAA GCT CCA GGA ATA TGT ATT GAT Lys Ile Gln Met Cys Lys Ser Val Lys Ala Pro Gly Ile Cys Ile Asp 435 440 445	1344
GTT GAT AAT GAA GAT TTG TTC TTT ATA GCT GAT AAA AAT AGT TTT TCA Val Asp Asn Glu Asp Leu Phe Phe Ile Ala Asp Lys Asn Ser Phe Ser 450 455 460	1392
GAT GAT TTA TCT AAA AAC GAA AGA ATA GAA TAT AAT ACA CAG AGT AAT Asp Asp Leu Ser Lys Asn Glu Arg Ile Glu Tyr Asn Thr Gln Ser Asn 465 470 475 480	1440
TAT ATA GAA AAT GAC TTC CCT ATA AAT GAA TTA ATT TTA GAT ACT GAT Tyr Ile Glu Asn Asp Phe Pro Ile Asn Glu Leu Ile Leu Asp Thr Asp 485 490 495	1488

TTA ATA AGT AAA ATA GAA TTA CCA AGT GAA AAT ACA GAA TCA CTT ACT Leu Ile Ser Lys Ile Glu Leu Pro Ser Glu Asn Thr Glu Ser Leu Thr 500	505	510	1536
GAT TTT AAT GTA GAT GTT CCA GTA TAT GAA AAA CAA CCC GCT ATA AAA Asp Phe Asn Val Asp Val Pro Val Tyr Glu Lys Gln Pro Ala Ile Lys 515	520	525	1584
AAA ATT TTT ACA GAT GAA AAT ACC ATC TTT CAA TAT TTA TAC TCT CAG Lys Ile Phe Thr Asp Glu Asn Thr Ile Phe Gln Tyr Leu Tyr Ser Gln 530	535	540	1632
ACA TTT CTC TTA GAT ATA AGA GAT ATA AGT TTA ACA TCT TCA TTT GAT Thr Phe Leu Leu Asp Ile Arg Asp Ile Ser Leu Thr Ser Ser Phe Asp 545	550	555	1680
GAT GCA TTA TTA TTT TCT AAC AAA GTT TAT TCA TTT TTT TCT ATG GAT Asp Ala Leu Leu Phe Ser Asn Lys Val Tyr Ser Phe Phe Ser Met Asp 565	570	575	1728
TAT ATT AAA ACT GCT AAT AAA GTG GTA GAA GCA GGA TTA TTT GCA GGT Tyr Ile Lys Thr Ala Asn Lys Val Val Glu Ala Gly Leu Phe Ala Gly 580	585	590	1776
TGG GTG AAA CAG ATA GTA AAT GAT TTT GTA ATC GAA GCT AAT AAA AGC Trp Val Lys Gln Ile Val Asn Asp Phe Val Ile Glu Ala Asn Lys Ser 595	600	605	1824
AAT ACT ATG GAT AAA ATT GCA GAT ATA TCT CTA ATT GTT CCT TAT ATA Asn Thr Met Asp Lys Ile Ala Asp Ile Ser Leu Ile Val Pro Tyr Ile 610	615	620	1872
GGA TTA GCT TTA AAT GTA GGA AAT GAA ACA GCT AAA GGA AAT TTT GAA Gly Leu Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Gly Asn Phe Glu 625	630	635	1920
AAT GCT TTT GAG ATT GCA GGA GCC AGT ATT CTA CTA GAA TTT ATA CCA Asn Ala Phe Glu Ile Ala Gly Ala Ser Ile Leu Leu Glu Phe Ile Pro 645	650	655	1968
GAA CTT TTA ATA CCT GTA GTT GGA GCC TTT TTA TTA GAA TCA TAT ATT Glu Leu Leu Ile Pro Val Val Gly Ala Phe Leu Leu Glu Ser Tyr Ile 660	665	670	2016
GAC AAT AAA AAT AAA ATT ATT AAA ACA ATA GAT AAT GCT TTA ACT AAA Asp Asn Lys Asn Lys Ile Ile Lys Thr Ile Asp Asn Ala Leu Thr Lys 675	680	685	2064
AGA AAT GAA AAA TGG AGT GAT ATG TAC GGA TTA ATA GTA GCG CAA TGG Arg Asn Glu Lys Trp Ser Asp Met Tyr Gly Leu Ile Val Ala Gln Trp 690	695	700	2112
CTC TCA ACA GTT AAT ACT CAA TTT TAT ACA ATA AAA GAG GGA ATG TAT Leu Ser Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Gly Met Tyr 705	710	715	2160
AAG GCT TTA AAT TAT CAA GCA CAA GCA TTG GAA GAA ATA ATA AAA TAC Lys Ala Leu Asn Tyr Gln Ala Gln Ala Leu Glu Glu Ile Ile Lys Tyr 725	730	735	2208

AGA TAT AAT ATA TAT TCT GAA AAA GAA AAG TCA AAT ATT AAC ATC GAT Arg Tyr Asn Ile Tyr Ser Glu Lys Glu Lys Ser Asn Ile Asn Ile Asp 740 745 750	2256
TTT AAT GAT ATA AAT TCT AAA CTT AAT GAG GGT ATT AAC CAA GCT ATA Phe Asn Asp Ile Asn Ser Lys Leu Asn Glu Gly Ile Asn Gln Ala Ile 755 760 765	2304
GAT AAT ATA AAT AAT TTT ATA AAT GGA TGT TCT GTA TCA TAT TTA ATG Asp Asn Ile Asn Asn Phe Ile Asn Gly Cys Ser Val Ser Tyr Leu Met 770 775 780	2352
AAA AAA ATG ATT CCA TTA GCT GTA GAA AAA TTA CTA GAC TTT GAT AAT Lys Lys Met Ile Pro Leu Ala Val Glu Lys Leu Leu Asp Phe Asp Asn 785 790 795 800	2400
ACT CTC AAA AAA AAT TTG TTA AAT TAT ATA GAT GAA AAT AAA TTA TAT Thr Leu Lys Lys Asn Leu Leu Asn Tyr Ile Asp Glu Asn Lys Leu Tyr 805 810 815	2448
TTG ATT GGA AGT GCA GAA TAT GAA AAA TCA AAA GTA AAT AAA TAC TTG Leu Ile Gly Ser Ala Glu Tyr Glu Lys Ser Lys Val Asn Lys Tyr Leu 820 825 830	2496
AAA ACC ATT ATG CCG TTT GAT CTT TCA ATA TAT ACC AAT GAT ACA ATA Lys Thr Ile Met Pro Phe Asp Leu Ser Ile Tyr Thr Asn Asp Thr Ile 835 840 845	2544
CTA ATA GAA ATG TTT AAT AAA TAT AAT AGC GAA ATT TTA AAT AAT ATT Leu Ile Glu Met Phe Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile 850 855 860	2592
ATC TTA AAT TTA AGA TAT AAG GAT AAT AAT TTA ATA GAT TTA TCA GGA Ile Leu Asn Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly 865 870 875 880	2640
TAT GGG GCA AAG GTA GAG GTA TAT GAT GGA GTC GAG CTT AAT GAT AAA Tyr Gly Ala Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys 885 890 895	2688
AAT CAA TTT AAA TTA ACT AGT TCA GCA AAT AGT AAG ATT AGA GTG ACT Asn Gln Phe Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr 900 905 910	2736
CAA AAT CAG AAT ATC ATA TTT AAT AGT GTG TTC CTT GAT TTT AGC GTT Gln Asn Gln Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val 915 920 925	2784
AGC TTT TGG ATA AGA ATA CCT AAA TAT AAG AAT GAT GGT ATA CAA AAT Ser Phe Trp Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn 930 935 940	2832
TAT ATT CAT AAT GAA TAT ACA ATA ATT AAT TGT ATG AAA AAT AAT TCG Tyr Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser 945 950 955 960	2880
GGC TGG AAA ATA TCT ATT AGG GGT AAT AGG ATA ATA TGG ACT TTA ATT Gly Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile 965 970 975	2928

GAT ATA AAT GGA AAA ACC AAA TCG GTA TTT TTT GAA TAT AAC ATA AGA Asp Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg 980 985 990	2976
GAA GAT ATA TCA GAG TAT ATA AAT AGA TGG TTT TTT GTA ACT ATT ACT Glu Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr 995 1000 1005	3024
AAT AAT TTG AAT AAC GCT AAA ATT TAT ATT AAT GGT AAG CTA GAA TCA Asn Asn Leu Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser 1010 1015 1020	3072
AAT ACA GAT ATT AAA GAT ATA AGA GAA GTT ATT GCT AAT GGT GAA ATA Asn Thr Asp Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile 1025 1030 1035 1040	3120
ATA TTT AAA TTA GAT GGT GAT ATA GAT AGA ACA CAA TTT ATT TGG ATG Ile Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met 1045 1050 1055	3168
AAA TAT TTC AGT ATT TTT AAT ACG GAA TTA AGT CAA TCA AAT ATT GAA Lys Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu 1060 1065 1070	3216
GAA AGA TAT AAA ATT CAA TCA TAT AGC GAA TAT TTA AAA GAT TTT TGG Glu Arg Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp 1075 1080 1085	3264
GGA AAT CCT TTA ATG TAC AAT AAA GAA TAT TAT ATG TTT AAT GCG GGG Gly Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly 1090 1095 1100	3312
AAT AAA AAT TCA TAT ATT AAA CTA AAG AAA GAT TCA CCT GTA GGT GAA Asn Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu 1105 1110 1115 1120	3360
ATT TTA ACA CGT AAA TAT AAT CAA AAT TCT AAA TAT ATA AAT ATT Ile Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr 1125 1130 1135	3408
AGA GAT TTA TAT ATT GGA GAA AAA TTT ATT ATA AGA AGA AAG TCA AAT Arg Asp Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn 1140 1145 1150	3456
TCT CAA TCT ATA AAT GAT GAT ATA GTT AGA AAA GAA GAT TAT ATA TAT Ser Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr 1155 1160 1165	3504
CTA GAT TTT TTT AAT TTA AAT CAA GAG TGG AGA GTA TAT ACC TAT AAA Leu Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys 1170 1175 1180	3552
TAT TTT AAG AAA GAG GAA GAA AAA TTG TTT TTA GCT CCT ATA AGT GAT Tyr Phe Lys Lys Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp 1185 1190 1195 1200	3600
TCT GAT GAG TTT TAC AAT ACT ATA CAA ATA AAA GAA TAT GAT GAA CAG Ser Asp Glu Phe Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln 1205 1210 1215	3648

CCA ACA TAT AGT TGT CAG TTG CTT TTT AAA AAA GAT GAA GAA AGT ACT	3696
Pro Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr	
1220 1225 1230	
GAT GAG ATA GGA TTG ATT GGT ATT CAT CGT TTC TAC GAA TCT GGA ATT	3744
Asp Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile	
1235 1240 1245	
GTA TTT GAA GAG TAT AAA GAT TAT TTT TGT ATA AGT AAA TGG TAC TTA	3792
Val Phe Glu Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu	
1250 1255 1260	
AAA GAG GTA AAA AGG AAA CCA TAT AAT TTA AAA TTG GGA TGT AAT TGG	3840
Lys Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp	
1265 1270 1275 1280	
CAG TTT ATT CCT AAA GAT GAA GGG TGG ACT GAA TAA	3876
Gln Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu	
1285 1290	

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1291 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Pro Val Thr Ile Asn Asn Phe Asn Tyr Asn Asp Pro Ile Asp Asn	
1 5 10 15	
Asn Asn Ile Ile Met Met Glu Pro Pro Phe Ala Arg Gly Thr Gly Arg	
20 25 30	
Tyr Tyr Lys Ala Phe Lys Ile Thr Asp Arg Ile Trp Ile Ile Pro Glu	
35 40 45	
Arg Tyr Thr Phe Gly Tyr Lys Pro Glu Asp Phe Asn Lys Ser Ser Gly	
50 55 60	
Ile Phe Asn Arg Asp Val Cys Glu Tyr Tyr Asp Pro Asp Tyr Leu Asn	
65 70 75 80	
Thr Asn Asp Lys Lys Asn Ile Phe Leu Gln Thr Met Ile Lys Leu Phe	
85 90 95	
Asn Arg Ile Lys Ser Lys Pro Leu Gly Glu Lys Leu Leu Glu Met Ile	
100 105 110	
Ile Asn Gly Ile Pro Tyr Leu Gly Asp Arg Arg Val Pro Leu Glu Glu	
115 120 125	
Phe Asn Thr Asn Ile Ala Ser Val Thr Val Asn Lys Leu Ile Ser Asn	
130 135 140	
Pro Gly Glu Val Glu Arg Lys Lys Gly Ile Phe Ala Asn Leu Ile Ile	
145 150 155 160	

Phe Gly Pro Gly Pro Val Leu Asn Glu Asn Glu Thr Ile Asp Ile Gly  
 165 170 175  
 Ile Gln Asn His Phe Ala Ser Arg Glu Gly Phe Gly Gly Ile Met Gln  
 180 185 190  
 Met Lys Phe Cys Pro Glu Tyr Val Ser Val Phe Asn Asn Val Gln Glu  
 195 200 205  
 Asn Lys Gly Ala Ser Ile Phe Asn Arg Arg Gly Tyr Phe Ser Asp Pro  
 210 215 220  
 Ala Leu Ile Leu Met His Glu Leu Ile His Val Leu His Gly Leu Tyr  
 225 230 235 240  
 Gly Ile Lys Val Asp Asp Leu Pro Ile Val Pro Asn Glu Lys Lys Phe  
 245 250 255  
 Phe Met Gln Ser Thr Asp Ala Ile Gln Ala Glu Glu Leu Tyr Thr Phe  
 260 265 270  
 Gly Gly Gln Asp Pro Ser Ile Ile Thr Pro Ser Thr Asp Lys Ser Ile  
 275 280 285  
 Tyr Asp Lys Val Leu Gln Asn Phe Arg Gly Ile Val Asp Arg Leu Asn  
 290 295 300  
 Lys Val Leu Val Cys Ile Ser Asp Pro Asn Ile Asn Ile Asn Ile Tyr  
 305 310 315 320  
 Lys Asn Lys Phe Lys Asp Lys Tyr Lys Phe Val Glu Asp Ser Glu Gly  
 325 330 335  
 Lys Tyr Ser Ile Asp Val Glu Ser Phe Asp Lys Leu Tyr Lys Ser Leu  
 340 345 350  
 Met Phe Gly Phe Thr Glu Thr Asn Ile Ala Glu Asn Tyr Lys Ile Lys  
 355 360 365  
 Thr Arg Ala Ser Tyr Phe Ser Asp Ser Leu Pro Pro Val Lys Ile Lys  
 370 375 380  
 Asn Leu Leu Asp Asn Glu Ile Tyr Thr Ile Glu Glu Gly Phe Asn Ile  
 385 390 395 400  
 Ser Asp Lys Asp Met Glu Lys Glu Tyr Arg Gly Gln Asn Lys Ala Ile  
 405 410 415  
 Asn Lys Gln Ala Tyr Glu Glu Ile Ser Lys Glu His Leu Ala Val Tyr  
 420 425 430  
 Lys Ile Gln Met Cys Lys Ser Val Lys Ala Pro Gly Ile Cys Ile Asp  
 435 440 445  
 Val Asp Asn Glu Asp Leu Phe Phe Ile Ala Asp Lys Asn Ser Phe Ser  
 450 455 460  
 Asp Asp Leu Ser Lys Asn Glu Arg Ile Glu Tyr Asn Thr Gln Ser Asn  
 465 470 475 480  
 Tyr Ile Glu Asn Asp Phe Pro Ile Asn Glu Leu Ile Leu Asp Thr Asp  
 485 490 495

Leu Ile Ser Lys Ile Glu Leu Pro Ser Glu Asn Thr Glu Ser Leu Thr  
 500 505 510  
 Asp Phe Asn Val Asp Val Pro Val Tyr Glu Lys Gln Pro Ala Ile Lys  
 515 520 525  
 Lys Ile Phe Thr Asp Glu Asn Thr Ile Phe Gln Tyr Leu Tyr Ser Gln  
 530 535 540  
 Thr Phe Leu Leu Asp Ile Arg Asp Ile Ser Leu Thr Ser Ser Phe Asp  
 545 550 555 560  
 Asp Ala Leu Leu Phe Ser Asn Lys Val Tyr Ser Phe Phe Ser Met Asp  
 565 570 575  
 Tyr Ile Lys Thr Ala Asn Lys Val Val Glu Ala Gly Leu Phe Ala Gly  
 580 585 590  
 Trp Val Lys Gln Ile Val Asn Asp Phe Val Ile Glu Ala Asn Lys Ser  
 595 600 605  
 Asn Thr Met Asp Lys Ile Ala Asp Ile Ser Leu Ile Val Pro Tyr Ile  
 610 615 620  
 Gly Leu Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Gly Asn Phe Glu  
 625 630 635 640  
 Asn Ala Phe Glu Ile Ala Gly Ala Ser Ile Leu Leu Glu Phe Ile Pro  
 645 650 655  
 Glu Leu Leu Ile Pro Val Val Gly Ala Phe Leu Leu Glu Ser Tyr Ile  
 660 665 670  
 Asp Asn Lys Asn Lys Ile Ile Lys Thr Ile Asp Asn Ala Leu Thr Lys  
 675 680 685  
 Arg Asn Glu Lys Trp Ser Asp Met Tyr Gly Leu Ile Val Ala Gln Trp  
 690 695 700  
 Leu Ser Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Gly Met Tyr  
 705 710 715 720  
 Lys Ala Leu Asn Tyr Gln Ala Gln Ala Leu Glu Glu Ile Ile Lys Tyr  
 725 730 735  
 Arg Tyr Asn Ile Tyr Ser Glu Lys Glu Lys Ser Asn Ile Asn Ile Asp  
 740 745 750  
 Phe Asn Asp Ile Asn Ser Lys Leu Asn Glu Gly Ile Asn Gln Ala Ile  
 755 760 765  
 Asp Asn Ile Asn Asn Phe Ile Asn Gly Cys Ser Val Ser Tyr Leu Met  
 770 775 780  
 Lys Lys Met Ile Pro Leu Ala Val Glu Lys Leu Leu Asp Phe Asp Asn  
 785 790 795 800  
 Thr Leu Lys Lys Asn Leu Leu Asn Tyr Ile Asp Glu Asn Lys Leu Tyr  
 805 810 815  
 Leu Ile Gly Ser Ala Glu Tyr Glu Lys Ser Lys Val Asn Lys Tyr Leu  
 820 825 830

Lys Thr Ile Met Pro Phe Asp Leu Ser Ile Tyr Thr Asn Asp Thr Ile  
 835 840 845  
 Leu Ile Glu Met Phe Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile  
 850 855 860  
 Ile Leu Asn Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly  
 865 870 875 880  
 Tyr Gly Ala Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys  
 885 890 895  
 Asn Gln Phe Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr  
 900 905 910  
 Gln Asn Gln Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val  
 915 920 925  
 Ser Phe Trp Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn  
 930 935 940  
 Tyr Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser  
 945 950 955 960  
 Gly Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile  
 965 970 975  
 Asp Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg  
 980 985 990  
 Glu Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr  
 995 1000 1005  
 Asn Asn Leu Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser  
 1010 1015 1020  
 Asn Thr Asp Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile  
 1025 1030 1035 1040  
 Ile Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met  
 1045 1050 1055  
 Lys Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu  
 1060 1065 1070  
 Glu Arg Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp  
 1075 1080 1085  
 Gly Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly  
 1090 1095 1100  
 Asn Lys Asn Ser Tyr Ile Lys Leu Lys Asp Ser Pro Val Gly Glu  
 1105 1110 1115 1120  
 Ile Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr  
 1125 1130 1135  
 Arg Asp Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn  
 1140 1145 1150  
 Ser Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr  
 1155 1160 1165

Leu Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys  
 1170 1175 1180 1181  
 Tyr Phe Lys Lys Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp  
 1185 1190 1195 1200  
 Ser Asp Glu Phe Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln  
 1205 1210 1215  
 Pro Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr  
 1220 1225 1230  
 Asp Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile  
 1235 1240 1245  
 Val Phe Glu Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu  
 1250 1255 1260  
 Lys Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp  
 1265 1270 1275 1280  
 Gln Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu  
 1285 1290

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1526 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 108..1523
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AGATCTCGAT CCCGCGAAAT TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA	60
TTCCCCCTCTA GAAATAATTT TGTTTAACCT TAAGAAGGAG ATATACC ATG GGC CAT Met Gly His 1	116
CAT CAT CAT CAT CAT CAT CAC AGC AGC GGC CAT ATC GAA GGT His His His His His His Ser Ser Gly His Ile Glu Gly 5 10 15	164
CGT CAT ATG GCT AGC ATG GCT GAT ACA ATA CTA ATA GAA ATG TTT AAT Arg His Met Ala Ser Met Ala Asp Thr Ile Leu Ile Glu Met Phe Asn 20 25 30 35	212
AAA TAT AAT AGC GAA ATT TTA AAT ATT ATC TTA AAT TTA AGA TAT Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn Leu Arg Tyr 40 45 50	260
AGA GAT AAT AAT TTA ATA GAT TTA TCA GGA TAT GGA GCA AAG GTA GAG Arg Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala Lys Val Glu 55 60 65	308

GTA TAT GAT GGG GTC AAG CTT AAT GAT AAA AAT CAA TTT AAA TTA ACT Val Tyr Asp Gly Val Lys Leu Asn Asp Lys Asn Gln Phe Lys Leu Thr 70 75 80	356
AGT TCA GCA GAT AGT AAG ATT AGA GTC ACT CAA AAT CAG AAT ATT ATA Ser Ser Ala Asp Ser Lys Ile Arg Val Thr Gln Asn Gln Asn Ile Ile 85 90 95	404
TTT AAT AGT ATG TTC CTT GAT TTT AGC GTT AGC TTT TGG ATA AGG ATA Phe Asn Ser Met Phe Leu Asp Phe Ser Val Ser Phe Trp Ile Arg Ile 100 105 110 115	452
CCT AAA TAT AGG AAT GAT GAT ATA CAA AAT TAT ATT CAT AAT GAA TAT Pro Lys Tyr Arg Asn Asp Asp Ile Gln Asn Tyr Ile His Asn Glu Tyr 120 125 130	500
ACG ATA ATT AAT TGT ATG AAA AAT AAT TCA GGC TGG AAA ATA TCT ATT Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys Ile Ser Ile 135 140 145	548
AGG GGT AAT AGG ATA ATA TGG ACC TTA ATT GAT ATA AAT GGA AAA ACC Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Ile Asn Gly Lys Thr 150 155 160	596
AAA TCA GTA TTT TTT GAA TAT AAC ATA AGA GAA GAT ATA TCA GAG TAT Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile Ser Glu Tyr 165 170 175	644
ATA AAT AGA TGG TTT TTT GTA ACT ATT ACT AAT AAT TTG GAT AAT GCT Ile Asn Arg Trp Phe Val Thr Ile Thr Asn Asn Leu Asp Asn Ala 180 185 190 195	692
AAA ATT TAT ATT AAT GGC ACG TTA GAA TCA AAT ATG GAT ATT AAA GAT Lys Ile Tyr Ile Asn Gly Thr Leu Glu Ser Asn Met Asp Ile Lys Asp 200 205 210	740
ATA GGA GAA GTT ATT GTT AAT GGT GAA ATA ACA TTT AAA TTA GAT GGT Ile Gly Glu Val Ile Val Asn Gly Glu Ile Thr Phe Lys Leu Asp Gly 215 220 225	788
GAT GTA GAT AGA ACA CAA TTT ATT TGG ATG AAA TAT TTT AGT ATT TTT Asp Val Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe Ser Ile Phe 230 235 240	836
AAT ACG CAA TTA AAT CAA TCA AAT ATT AAA GAG ATA TAT AAA ATT CAA Asn Thr Gln Leu Asn Gln Ser Asn Ile Lys Glu Ile Tyr Lys Ile Gln 245 250 255	884
TCA TAT AGC GAA TAC TTA AAA GAT TTT TGG GGA AAT CCT TTA ATG TAT Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro Leu Met Tyr 260 265 270 275	932
AAT AAA GAA TAT TAT ATG TTT AAT GCG GGG AAT AAA AAT TCA TAT ATT Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn Ser Tyr Ile 280 285 290	980
AAA CTA GTG AAA GAT TCA TCT GTA GGT GAA ATA TTA ATA CGT AGC AAA Lys Leu Val Lys Asp Ser Ser Val Gly Glu Ile Leu Ile Arg Ser Lys 295 300 305	1028

TAT AAT CAG AAT TCC AAT TAT ATA AAT TAT AGA AAT TTA TAT ATT GGA Tyr Asn Gln Asn Ser Asn Tyr Ile Asn Tyr Arg Asn Leu Tyr Ile Gly 310 315 320	1076
GAA AAA TTT ATT ATA AGA AGA GAG TCA AAT TCT CAA TCT ATA AAT GAT Glu Lys Phe Ile Ile Arg Arg Glu Ser Asn Ser Gln Ser Ile Asn Asp 325 330 335	1124
GAT ATA GTT AGA AAA GAA GAT TAT ATA CAT CTA GAT TTG GTA CTT CAC Asp Ile Val Arg Lys Glu Asp Tyr Ile His Leu Asp Leu Val Leu His 340 345 350 355	1172
CAT GAA GAG TGG AGA GTA TAT GCC TAT AAA TAT TTT AAG GAA CAG GAA His Glu Glu Trp Arg Val Tyr Ala Tyr Lys Tyr Phe Lys Glu Gln Glu 360 365 370	1220
GAA AAA TTG TTT TTA TCT ATT ATA AGT GAT TCT AAT GAA TTT TAT AAG Glu Lys Leu Phe Leu Ser Ile Ile Ser Asp Ser Asn Glu Phe Tyr Lys 375 380 385	1268
ACT ATA GAA ATA AAA GAA TAT GAT GAA CAG CCA TCA TAT AGT TGT CAG Thr Ile Glu Ile Lys Glu Tyr Asp Glu Gln Pro Ser Tyr Ser Cys Gln 390 395 400	1316
TTG CTT TTT AAA AAA GAT GAA GAA AGT ACT GAT GAT ATA GGA TTG ATT Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Asp Ile Gly Leu Ile 405 410 415	1364
GGT ATT CAT CGT TTC TAC GAA TCT GGA GTT TTA CGT AAA AAG TAT AAA Gly Ile His Arg Phe Tyr Glu Ser Gly Val Leu Arg Lys Lys Tyr Lys 420 425 430 435	1412
GAT TAT TTT TGT ATA AGT AAA TGG TAC TTA AAA GAG GTA AAA AGG AAA Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val Lys Arg Lys 440 445 450	1460
CCA TAT AAG TCA AAT TTG GGA TGT AAT TGG CAG TTT ATT CCT AAA GAT Pro Tyr Lys Ser Asn Leu Gly Cys Asn Trp Gln Phe Ile Pro Lys Asp 455 460 465	1508
GAA GGG TGG ACT GAA TAA Glu Gly Trp Thr Glu 470	1526

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 472 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- ii) MOLECULE TYPE: protein
- iii) SEQUENCE DESCRIPTION: SEQ ID N

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Met Gly His His His His His His His His Ser Ser Gly His
      1           5           10          15

Ile Glu Gly Arg His Met Ala Ser Met Ala Asp Thr Ile Leu Ile Glu
      20          25          30

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Met Phe Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn  
           35                        40                                45  
 Leu Arg Tyr Arg Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala  
           50                        55                                60  
 Lys Val Glu Val Tyr Asp Gly Val Lys Leu Asn Asp Lys Asn Gln Phe  
           65                        70                                75                        80  
 Lys Leu Thr Ser Ser Ala Asp Ser Lys Ile Arg Val Thr Gln Asn Gln  
           85                        90                                95  
 Asn Ile Ile Phe Asn Ser Met Phe Leu Asp Phe Ser Val Ser Phe Trp  
           100                       105                                110  
 Ile Arg Ile Pro Lys Tyr Arg Asn Asp Asp Ile Gln Asn Tyr Ile His  
           115                       120                                125  
 Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys  
           130                       135                                140  
 Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Ile Asn  
           145                       150                                155                        160  
 Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile  
           165                       170                                175  
 Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu  
           180                       185                                190  
 Asp Asn Ala Lys Ile Tyr Ile Asn Gly Thr Leu Glu Ser Asn Met Asp  
           195                       200                                205  
 Ile Lys Asp Ile Gly Glu Val Ile Val Asn Gly Glu Ile Thr Phe Lys  
           210                       215                                220  
 Leu Asp Gly Asp Val Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe  
           225                       230                                235                        240  
 Ser Ile Phe Asn Thr Gln Leu Asn Gln Ser Asn Ile Lys Glu Ile Tyr  
           245                       250                                255  
 Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro  
           260                       265                                270  
 Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn  
           275                       280                                285  
 Ser Tyr Ile Lys Leu Val Lys Asp Ser Ser Val Gly Glu Ile Leu Ile  
           290                       295                                300  
 Arg Ser Lys Tyr Asn Gln Asn Ser Asn Tyr Ile Asn Tyr Arg Asn Leu  
           305                       310                                315                        320  
 Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Glu Ser Asn Ser Gln Ser  
           325                       330                                335  
 Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile His Leu Asp Leu  
           340                       345                                350  
 Val Leu His His Glu Glu Trp Arg Val Tyr Ala Tyr Lys Tyr Phe Lys  
           355                       360                                365

Glu Gln Glu Glu Lys Leu Phe Leu Ser Ile Ile Ser Asp Ser Asn Glu  
 370 375 380  
 Phe Tyr Lys Thr Ile Glu Ile Lys Glu Tyr Asp Glu Gln Pro Ser Tyr  
 385 390 395 400  
 Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Asp Ile  
 405 410 415  
 Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Val Leu Arg Lys  
 420 425 430  
 Lys Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val  
 435 440 445  
 Lys Arg Lys Pro Tyr Lys Ser Asn Leu Gly Cys Asn Trp Gln Phe Ile  
 450 455 460  
 Pro Lys Asp Glu Gly Trp Thr Glu  
 465 470

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 108..1523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AGATCTCGAT CCCGCGAAAT TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA	60
TTCCCCCTCTA GAAATAATT TGTTTAACCT TAAGAAGGAG ATATACC ATG GGC CAT Met Gly His 1	116
CAT CAT CAT CAT CAT CAT CAC AGC AGC GGC CAT ATC GAA GGT His His His His His His Ser Ser Gly His Ile Glu Gly 5 10 15	164
CGT CAT ATG GCT AGC ATG GCT GAT ACA ATA CTA ATA GAA ATG TTT AAT Arg His Met Ala Ser Met Ala Asp Thr Ile Leu Ile Glu Met Phe Asn 20 25 30 35	212
AAA TAT AAT AGC GAA ATT TTA AAT ATT ATC TTA AAT TTA AGA TAT Lys Tyr Asn Ser Glu Ile Leu Asn Ile Ile Leu Asn Leu Arg Tyr 40 45 50	260
AAG GAT AAT AAT TTA ATA GAT TTA TCA GGA TAT GGG GCA AAG GTA GAG Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala Lys Val Glu 55 60 65	308
GTA TAT GAT GGA GTC GAG CTT AAT GAT AAA AAT CAA TTT AAA TTA ACT Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe Lys Leu Thr 70 75 80	356

AGT TCA GCA AAT AGT AAG ATT AGA GTG ACT CAA AAT CAG AAT ATC ATA Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln Asn Ile Ile 85 90 95	404
TTT AAT AGT GTG TTC CTT GAT TTT AGC GTT AGC TTT TGG ATA AGA ATA Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser Phe Trp Ile Arg Ile 100 105 110 115	452
CCT AAA TAT AAG AAT GAT GGT ATA CAA AAT TAT ATT CAT AAT GAA TAT Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr Ile His Asn Glu Tyr 120 125 130	500
ACA ATA ATT AAT TGT ATG AAA AAT AAT TCG GGC TGG AAA ATA TCT ATT Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys Ile Ser Ile 135 140 145	548
AGG GGT AAT AGG ATA ATA TGG ACT TTA ATT GAT ATA AAT GGA AAA ACC Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Ile Asn Gly Lys Thr 150 155 160	596
AAA TCG GTA TTT TTT GAA TAT AAC ATA AGA GAA GAT ATA TCA GAG TAT Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile Ser Glu Tyr 165 170 175	644
ATA AAT AGA TGG TTT TTT GTA ACT ATT ACT AAT AAT TTG AAT AAC GCT Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu Asn Asn Ala 180 185 190 195	692
AAA ATT TAT ATT AAT GGT AAG CTA GAA TCA AAT ACA GAT ATT AAA GAT Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp Ile Lys Asp 200 205 210	740
ATA AGA GAA GTT ATT GCT AAT GGT GAA ATA ATA TTT AAA TTA GAT GGT Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys Leu Asp Gly 215 220 225	788
GAT ATA GAT AGA ACA CAA TTT ATT TGG ATG AAA TAT TTC AGT ATT TTT Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe Ser Ile Phe 230 235 240	836
AAT ACG GAA TTA AGT CAA TCA AAT ATT GAA GAA AGA TAT AAA ATT CAA Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr Lys Ile Gln 245 250 255	884
TCA TAT AGC GAA TAT TTA AAA GAT TTT TGG GGA AAT CCT TTA ATG TAC Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro Leu Met Tyr 260 265 270 275	932
AAT AAA GAA TAT TAT ATG TTT AAT GCG GGG AAT AAA AAT TCA TAT ATT Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn Ser Tyr Ile 280 285 290	980
AAA CTA AAG AAA GAT TCA CCT GTA GGT GAA ATT TTA ACA CGT AGC AAA Lys Leu Lys Asp Ser Pro Val Gly Glu Ile Leu Thr Arg Ser Lys 295 300 305	1028
TAT AAT CAA AAT TCT AAA TAT ATA AAT TAT AGA GAT TTA TAT ATT GGA Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu Tyr Ile Gly 310 315 320	1076

GAA AAA TTT ATT ATA AGA AGA AAG TCA AAT TCT CAA TCT ATA AAT GAT Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser Ile Asn Asp 325                   330                   335	1124
GAT ATA GTT AGA AAA GAA GAT TAT ATA TAT CTA GAT TTT TTT AAT TTA Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe Phe Asn Leu 340                   345                   350                   355	1172
AAT CAA GAG TGG AGA GTA TAT ACC TAT AAA TAT TTT AAG AAA GAG GAA Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys Lys Glu Glu 360                   365                   370	1220
GAA AAA TTG TTT TTA GCT CCT ATA AGT GAT TCT GAT GAG TTT TAC AAT Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu Phe Tyr Asn 375                   380                   385	1268
ACT ATA CAA ATA AAA GAA TAT GAT GAA CAG CCA ACA TAT AGT TGT CAG Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr Ser Cys Gln 390                   395                   400	1316
TTG CTT TTT AAA AAA GAT GAA GAA AGT ACT GAT GAG ATA GGA TTG ATT Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile Gly Leu Ile 405                   410                   415	1364
GGT ATT CAT CGT TTC TAC GAA TCT GGA ATT GTA TTT GAA GAG TAT AAA Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu Glu Tyr Lys 420                   425                   430                   435	1412
GAT TAT TTT TGT ATA AGT AAA TGG TAC TTA AAA GAG GTA AAA AGG AAA Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val Lys Arg Lys 440                   445                   450	1460
CCA TAT AAT TTA AAA TTG GGA TGT AAT TGG CAG TTT ATT CCT AAA GAT Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile Pro Lys Asp 455                   460                   465	1508
GAA GGG TGG ACT GAA TAAAAGCTTG CGGCCGCACT CGAG Glu Gly Trp Thr Glu 470	1547

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 472 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Gly His His His His His His His His Ser Ser Gly His 1                   5                   10                   15
Ile Glu Gly Arg His Met Ala Ser Met Ala Asp Thr Ile Leu Ile Glu 20                   25                   30
Met Phe Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn 35                   40                   45
Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala 50                   55                   60

Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe  
 65 70 75 80

Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln  
 85 90 95

Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser Phe Trp  
 100 105 110

Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr Ile His  
 115 120 125

Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys  
 130 135 140

Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Ile Asn  
 145 150 155 160

Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile  
 165 170 175

Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu  
 180 185 190

Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp  
 195 200 205

Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys  
 210 215 220

Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe  
 225 230 235 240

Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr  
 245 250 255

Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro  
 260 265 270

Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn  
 275 280 285

Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Thr  
 290 295 300

Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu  
 305 310 315 320

Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser  
 325 330 335

Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe  
 340 345 350

Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys  
 355 360 365

Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu  
 370 375 380

Phe Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr  
 385 390 395 400

Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile  
405 410 415

Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu  
420 425 430

Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val  
435 440 445

Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile  
450 455 460

Pro Lys Asp Glu Gly Trp Thr Glu  
465 470

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CGCCATGGCT GATACAATAC TAATAGAAAT G

31

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCAAGCTTTT ATTCAAGTCCA CCCTTCATC

29

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3753 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..3750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATG CCA ACA ATT AAT AGT TTT AAT TAT AAT GAT CCT GTT AAT AAT AGA Met Pro Thr Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Asn Asn Arg	48
1 5 10 15	
ACA ATT TTA TAT ATT AAA CCA GGC GGT TGT CAA CAA TTT TAT AAA TCA Thr Ile Leu Tyr Ile Lys Pro Gly Gly Cys Gln Gln Phe Tyr Lys Ser	96
20 25 30	
TTT AAT ATT ATG AAA AAT ATT TGG ATA ATT CCA GAG AGA AAT GTA ATT Phe Asn Ile Met Lys Asn Ile Trp Ile Ile Pro Glu Arg Asn Val Ile	144
35 40 45	
GGT ACA ATT CCC CAA GAT TTT CTT CCG CCT ACT TCA TTG AAA AAT GGA Gly Thr Ile Pro Gln Asp Phe Leu Pro Pro Thr Ser Leu Lys Asn Gly	192
50 55 60	
GAT AGT AGT TAT TAT GAC CCT AAT TAT TTA CAA AGT GAT CAA GAA AAG Asp Ser Ser Tyr Tyr Asp Pro Asn Tyr Leu Gln Ser Asp Gln Glu Lys	240
65 70 75 80	
GAT AAA TTT TTA AAA ATA GTC ACA AAA ATA TTT AAT AGA ATA AAT GAT Asp Lys Phe Leu Lys Ile Val Thr Lys Ile Phe Asn Arg Ile Asn Asp	288
85 90 95	
AAT CTT TCA GGA AGG ATT TTA TTA GAA GAA CTG TCA AAA GCT AAT CCA Asn Leu Ser Gly Arg Ile Leu Leu Glu Leu Ser Lys Ala Asn Pro	336
100 105 110	
TAT TTA GGA AAT GAT AAT ACT CCA GAT GGT GAC TTC ATT ATT AAT GAT Tyr Leu Gly Asn Asp Asn Thr Pro Asp Gly Asp Phe Ile Ile Asn Asp	384
115 120 125	
GCA TCA GCA GTT CCA ATT CAA TTC TCA AAT GGT AGC CAA AGC ATA CTA Ala Ser Ala Val Pro Ile Gln Phe Ser Asn Gly Ser Gln Ser Ile Leu	432
130 135 140	
TTA CCT AAT GTT ATT ATA ATG GGA GCA GAG CCT GAT TTA TTT GAA ACT Leu Pro Asn Val Ile Ile Met Gly Ala Glu Pro Asp Leu Phe Glu Thr	480
145 150 155 160	
AAC AGT TCC AAT ATT TCT CTA AGA AAT AAT TAT ATG CCA AGC AAT CAC Asn Ser Ser Asn Ile Ser Leu Arg Asn Asn Tyr Met Pro Ser Asn His	528
165 170 175	
GGT TTT GGA TCA ATA GCT ATA GTA ACA TTC TCA CCT GAA TAT TCT TTT Gly Phe Gly Ser Ile Ala Ile Val Thr Phe Ser Pro Glu Tyr Ser Phe	576
180 185 190	
AGA TTT AAA GAT AAT AGT ATG AAT GAA TTT ATT CAA GAT CCT GCT CTT Arg Phe Lys Asp Asn Ser Met Asn Glu Phe Ile Gln Asp Pro Ala Leu	624
195 200 205	
ACA TTA ATG CAT GAA TTA ATA CAT TCA TTA CAT GGA CTA TAT GGG GCT Thr Leu Met His Glu Leu Ile His Ser Leu His Gly Leu Tyr Gly Ala	672
210 215 220	
AAA GGG ATT ACT ACA AAG TAT ACT ATA ACA CAA AAA CAA AAT CCC CTA Lys Gly Ile Thr Thr Lys Tyr Thr Ile Thr Gln Lys Gln Asn Pro Leu	720
225 230 235 240	

ATA ACA AAT ATA AGA GGT ACA AAT ATT GAA GAA TTC TTA ACT TTT GGA Ile Thr Asn Ile Arg Gly Thr Asn Ile Glu Glu Phe Leu Thr Phe Gly 245 250 255	768
GGT ACT GAT TTA AAC ATT ATT ACT AGT GCT CAG TCC AAT GAT ATC TAT Gly Thr Asp Leu Asn Ile Ile Thr Ser Ala Gln Ser Asn Asp Ile Tyr 260 265 270	816
ACT AAT CTT CTA GCT GAT TAT AAA AAA ATA GCG TCT AAA CTT AGC AAA Thr Asn Leu Leu Ala Asp Tyr Lys Lys Ile Ala Ser Lys Leu Ser Lys 275 280 285	864
GTA CAA GTA TCT AAT CCA CTA CTT AAT CCT TAT AAA GAT GTT TTT GAA Val Gln Val Ser Asn Pro Leu Leu Asn Pro Tyr Lys Asp Val Phe Glu 290 295 300	912
GCA AAG TAT GGA TTA GAT AAA GAT GCT AGC GGA ATT TAT TCG GTA AAT Ala Lys Tyr Gly Leu Asp Lys Asp Ala Ser Gly Ile Tyr Ser Val Asn 305 310 315 320	960
ATA AAC AAA TTT AAT GAT ATT TTT AAA AAA TTA TAC AGC TTT ACG GAA Ile Asn Lys Phe Asn Asp Ile Phe Lys Lys Leu Tyr Ser Phe Thr Glu 325 330 335	1008
TTT GAT TTA GCA ACT AAA TTT CAA GTT AAA TGT AGG CAA ACT TAT ATT Phe Asp Leu Ala Thr Lys Phe Gln Val Lys Cys Arg Gln Thr Tyr Ile 340 345 350	1056
GGA CAG TAT AAA TAC TTC AAA CTT TCA AAC TTG TTA AAT GAT TCT ATT Gly Gln Tyr Lys Tyr Phe Lys Leu Ser Asn Leu Leu Asn Asp Ser Ile 355 360 365	1104
TAT AAT ATA TCA GAA GGC TAT AAT ATA AAT AAT TTA AAG GTA AAT TTT Tyr Asn Ile Ser Glu Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe 370 375 380	1152
AGA GGA CAG AAT GCA AAT TTA AAT CCT AGA ATT ATT ACA CCA ATT ACA Arg Gly Gln Asn Ala Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Thr 385 390 395 400	1200
GGT AGA GGA CTA GTA AAA AAA ATC ATT AGA TTT TGT AAA AAT ATT GTT Gly Arg Gly Leu Val Lys Lys Ile Ile Arg Phe Cys Lys Asn Ile Val 405 410 415	1248
TCT GTA AAA GGC ATA AGG AAA TCA ATA TGT ATC GAA ATA AAT AAT GGT Ser Val Lys Gly Ile Arg Lys Ser Ile Cys Ile Glu Ile Asn Asn Gly 420 425 430	1296
SAG TTA TTT TTT GTG GCT TCC GAG AAT AGT TAT AAT GAT GAT AAT ATA Glu Leu Phe Phe Val Ala Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile 435 440 445	1344
AAT ACT CCT AAA GAA ATT GAC GAT ACA GTA ACT TCA AAT AAT AAT TAT Asn Thr Pro Lys Glu Ile Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr 450 455 460	1392
GAA AAT GAT TTA GAT CAG GTT ATT TTA AAT TTT AAT AGT GAA TCA GCA Glu Asn Asp Leu Asp Gln Val Ile Leu Asn Phe Asn Ser Glu Ser Ala 465 470 475 480	1440

CCT GGA CTT TCA GAT GAA AAA TTA AAT TTA ACT ATC CAA AAT GAT GCT Pro Gly Leu Ser Asp Glu Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala 485 490 495	1488
TAT ATA CCA AAA TAT GAT TCT AAT GGA ACA AGT GAT ATA GAA CAA CAT Tyr Ile Pro Lys Tyr Asp Ser Asn Gly Thr Ser Asp Ile Glu Gln His 500 505 510	1536
GAT GTT AAT GAA CTT AAT GTA TTT TTC TAT TTA GAT GCA CAG AAA GTG Asp Val Asn Glu Leu Asn Val Phe Phe Tyr Leu Asp Ala Gln Lys Val 515 520 525	1584
CCC GAA GGT GAA AAT AAT GTC AAT CTC ACC TCT TCA ATT GAT ACA GCA Pro Glu Gly Glu Asn Asn Val Asn Leu Thr Ser Ser Ile Asp Thr Ala 530 535 540	1632
TTA TTA GAA CAA CCT AAA ATA TAT ACA TTT TTT TCA TCA GAA TTT ATT Leu Leu Glu Gln Pro Lys Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile 545 550 555 560	1680
AAT AAT GTC AAT AAA CCT GTG CAA GCA GCA TTA TTT GTA AGC TGG ATA Asn Asn Val Asn Lys Pro Val Gln Ala Ala Leu Phe Val Ser Trp Ile 565 570 575	1728
CAA CAA GTA TTA GTA GAT TTT ACT ACT GAA GCT AAC CAA AAA AGT ACT Gln Gln Val Leu Val Asp Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr 580 585 590	1776
GTT GAT AAA ATT GCA GAT ATT TCT ATA GTT GTT CCA TAT ATA GGT CTT Val Asp Lys Ile Ala Asp Ile Ser Ile Val Val Pro Tyr Ile Gly Leu 595 600 605	1824
GCT TTA AAT ATA GGA AAT GAA GCA CAA AAA GGA AAT TTT AAA GAT GCA Ala Leu Asn Ile Gly Asn Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala 610 615 620	1872
CTT GAA TTA TTA GGA GCA GGT ATT TTA TTA GAA TTT GAA CCC GAG CTT Leu Glu Leu Leu Gly Ala Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu 625 630 635 640	1920
TTA ATT CCT ACA ATT TTA GTA TTC ACG ATA AAA TCT TTT TTA GGT TCA Leu Ile Pro Thr Ile Leu Val Phe Thr Ile Lys Ser Phe Leu Gly Ser 645 650 655	1968
TCT GAT AAT AAA AAT AAA GTT ATT AAA GCA ATA AAT AAT GCA TTG AAA Ser Asp Asn Lys Asn Lys Val Ile Lys Ala Ile Asn Asn Ala Leu Lys 660 665 670	2016
GAA AGA GAT GAA AAA TGG AAA GAA GTA TAT AGT TTT ATA GTA TCG AAT Glu Arg Asp Glu Lys Trp Lys Glu Val Tyr Ser Phe Ile Val Ser Asn 675 680 685	2064
TGG ATG ACT AAA ATT AAT ACA CAA TTT AAT AAA AGA AAA GAA CAA ATG Trp Met Thr Lys Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met 690 695 700	2112
TAT CAA GCT TTA CAA AAT CAA GTA AAT GCA CTT AAA GCA ATA ATA GAA Tyr Gln Ala Leu Gln Asn Gln Val Asn Ala Leu Lys Ala Ile Ile Glu 705 710 715 720	2160

TCT AAG TAT AAT AGT TAT ACT TTA GAA GAA AAA AAT GAG CTT ACA AAT Ser Lys Tyr Asn Ser Tyr Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn 725 730 735	2208
AAA TAT GAT ATT GAG CAA ATA GAA AAT GAA CTT AAT CAA AAG GTT TCT Lys Tyr Asp Ile Glu Gln Ile Glu Asn Glu Leu Asn Gln Lys Val Ser 740 745 750	2256
ATA GCA ATG AAT AAT ATA GAC AGG TTC TTA ACT GAA AGT TCT ATA TCT Ile Ala Met Asn Asn Ile Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser 755 760 765	2304
TAT TTA ATG AAA TTA ATA AAT GAA GTA AAA ATT AAT AAA TTA AGA GAA Tyr Leu Met Lys Leu Ile Asn Glu Val Lys Ile Asn Lys Leu Arg Glu 770 775 780	2352
TAT GAT GAA AAT GTT AAA ACG TAT TTA TTA GAT TAT ATT ATA AAA CAT Tyr Asp Glu Asn Val Lys Thr Tyr Leu Leu Asp Tyr Ile Ile Lys His 785 790 795 800	2400
GGA TCA ATC TTG GGA GAG AGT CAG CAA GAA CTA AAT TCT ATG GTA ATT Gly Ser Ile Leu Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Ile 805 810 815	2448
GAT ACC CTA AAT AAT AGT ATT CCT TTT AAG CTT TCT TCT TAT ACA GAT Asp Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp 820 825 830	2496
GAT AAA ATT TTA ATT TCA TAT TTT AAT AAG TTC TTT AAG AGA ATT AAA Asp Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys 835 840 845	2544
AGT AGT TCT GTT TTA AAT ATG AGA TAT AAA AAT GAT AAA TAC GTA GAT Ser Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp 850 855 860	2592
ACT TCA GGA TAT GAT TCA AAT ATA AAT ATT AAT GGA GAT GTA TAT AAA Thr Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys 865 870 875 880	2640
TAT CCA ACT AAT AAA AAT CAA TTT GGA ATA TAT AAT GAT AAA CTT AGT Tyr Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser 885 890 895	2688
GAA GTT AAT ATA TCT CAA AAT GAT TAC ATT ATA TAT GAT AAT AAA TAT Glu Val Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr 900 905 910	2736
AAA AAT TTT AGT ATT AGT TTT TGG GTA AGA ATT CCT AAC TAT GAT AAT Lys Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn 915 920 925	2784
AAG ATA GTA AAT GTT AAT AAT GAA TAC ACT ATA ATA AAT TGT ATG AGG Lys Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg 930 935 940	2832
GAT AAT AAT TCA GGA TGG AAA GTA TCT CTT AAT CAT AAT GAA ATA ATT Asp Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile 945 950 955 960	2880

TGG ACA TTG CAA GAT AAT TCA GGA ATT AAT CAA AAA TTA GCA TTT AAC Trp Thr Leu Gln Asp Asn Ser Gly Ile Asn Gln Lys Leu Ala Phe Asn 965 970 975	2928
TAT GGT AAC GCA AAT GGT ATT TCT GAT TAT ATA AAT AAG TGG ATT TTT Tyr Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe 980 985 990	2976
GTA ACT ATA ACT AAT GAT AGA TTA GGA GAT TCT AAA CTT TAT ATT AAT Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn 995 1000 1005	3024
GGA AAT TTA ATA GAT AAA AAA TCA ATT TTA AAT TTA GGT AAT ATT CAT Gly Asn Leu Ile Asp Lys Lys Ser Ile Leu Asn Leu Gly Asn Ile His 1010 1015 1020	3072
GTT AGT GAC AAT ATA TTA TTT AAA ATA GTT AAT TGT AGT TAT ACA AGA Val Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg 1025 1030 1035 1040	3120
TAT ATT GGT ATT AGA TAT TTT AAT ATT TTT GAT AAA GAA TTA GAT GAA Tyr Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu 1045 1050 1055	3168
ACA GAA ATT CAA ACT TTA TAT AAC AAT GAA CCT AAT GCA AAT ATT TTA Thr Glu Ile Gln Thr Leu Tyr Asn Asn Glu Pro Asn Ala Asn Ile Leu 1060 1065 1070	3216
AAG GAT TTT TGG GGA AAT TAT TTG CTT TAT GAC AAA GAA TAC TAT TTA Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu 1075 1080 1085	3264
TTA AAT GTG TTA AAA CCA AAT AAC TTT ATT AAT AGG AGA ACA GAT TCT Leu Asn Val Leu Lys Pro Asn Asn Phe Ile Asn Arg Arg Thr Asp Ser 1090 1095 1100	3312
ACT TTA AGC ATT AAT AAT ATA AGA AGC ACT ATT CTT TTA GCT AAT AGA Thr Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg 1105 1110 1115 1120	3360
TTA TAT AGT GGA ATA AAA GTT AAA ATA CAA AGA GTT AAT AAT AGT AGT Leu Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser 1125 1130 1135	3408
ACT AAC GAT AAT CTT GTT AGA AAG AAT GAT CAG GTA TAT ATT AAT TTT Thr Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe 1140 1145 1150	3456
GTA GCC AGC AAA ACT CAC TTA CTT CCA TTA TAT GCT GAT ACA GCT ACC Val Ala Ser Lys Thr His Leu Leu Pro Leu Tyr Ala Asp Thr Ala Thr 1155 1160 1165	3504
ACA AAT AAA GAG AAA ACA ATA AAA ATA TCA TCA TCT GGC AAT AGA TTT Thr Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe 1170 1175 1180	3552
AAT CAA GTA GTA GTT ATG AAT TCA GTA GGA TGT ACA ATG AAT TTT AAA Asn Gln Val Val Val Met Asn Ser Val Gly Cys Thr Met Asn Phe Lys 1185 1190 1195 1200	3600

AAT AAT AAT GGA AAT AAT ATT GGG TTG TTA GGT TTC AAG GCA GAT ACT Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp Thr 1205 1210 1215	3648
GTA GTT GCT AGT ACT TGG TAT TAT ACA CAT ATG AGA GAT AAT ACA AAC Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp Asn Thr Asn 1220 1225 1230	3696
AGC AAT GGA TTT TTT TGG AAC TTT ATT TCT GAA GAA CAT GGA TGG CAA Ser Asn Gly Phe Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp Gln 1235 1240 1245	3744
GAA AAA TAA Glu Lys 1250	3753

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1250 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Pro Thr Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Asn Asn Arg 1 5 10 15
Thr Ile Leu Tyr Ile Lys Pro Gly Gly Cys Gln Gln Phe Tyr Lys Ser 20 25 30
Phe Asn Ile Met Lys Asn Ile Trp Ile Ile Pro Glu Arg Asn Val Ile 35 40 45
Gly Thr Ile Pro Gln Asp Phe Leu Pro Pro Thr Ser Leu Lys Asn Gly 50 55 60
Asp Ser Ser Tyr Tyr Asp Pro Asn Tyr Leu Gln Ser Asp Gln Glu Lys 65 70 75 80
Asp Lys Phe Leu Lys Ile Val Thr Lys Ile Phe Asn Arg Ile Asn Asp 85 90 95
Asn Leu Ser Gly Arg Ile Leu Leu Glu Glu Leu Ser Lys Ala Asn Pro 100 105 110
Tyr Leu Gly Asn Asp Asn Thr Pro Asp Gly Asp Phe Ile Ile Asn Asp 115 120 125
Ala Ser Ala Val Pro Ile Gln Phe Ser Asn Gly Ser Gln Ser Ile Leu 130 135 140
Leu Pro Asn Val Ile Ile Met Gly Ala Glu Pro Asp Leu Phe Glu Thr 145 150 155 160
Asn Ser Ser Asn Ile Ser Leu Arg Asn Asn Tyr Met Pro Ser Asn His 165 170 175
Gly Phe Gly Ser Ile Ala Ile Val Thr Phe Ser Pro Glu Tyr Ser Phe 180 185 190

Arg Phe Lys Asp Asn Ser Met Asn Glu Phe Ile Gln Asp Pro Ala Leu  
195 200 205

Thr Leu Met His Glu Leu Ile His Ser Leu His Gly Leu Tyr Gly Ala  
210 215 220

Lys Gly Ile Thr Thr Lys Tyr Thr Ile Thr Gln Lys Gln Asn Pro Leu  
225 230 235 240

Ile Thr Asn Ile Arg Gly Thr Asn Ile Glu Glu Phe Leu Thr Phe Gly  
245 250 255

Gly Thr Asp Leu Asn Ile Ile Thr Ser Ala Gln Ser Asn Asp Ile Tyr  
260 265 270

Thr Asn Leu Leu Ala Asp Tyr Lys Lys Ile Ala Ser Lys Leu Ser Lys  
275 280 285

Val Gln Val Ser Asn Pro Leu Leu Asn Pro Tyr Lys Asp Val Phe Glu  
290 295 300

Ala Lys Tyr Gly Leu Asp Lys Asp Ala Ser Gly Ile Tyr Ser Val Asn  
305 310 315 320

Ile Asn Lys Phe Asn Asp Ile Phe Lys Lys Leu Tyr Ser Phe Thr Glu  
325 330 335

Phe Asp Leu Ala Thr Lys Phe Gln Val Lys Cys Arg Gln Thr Tyr Ile  
340 345 350

Gly Gln Tyr Lys Tyr Phe Lys Leu Ser Asn Leu Leu Asn Asp Ser Ile  
355 360 365

Tyr Asn Ile Ser Glu Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe  
370 375 380

Arg Gly Gln Asn Ala Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Thr  
385 390 395 400

Gly Arg Gly Leu Val Lys Lys Ile Ile Arg Phe Cys Lys Asn Ile Val  
405 410 415

Ser Val Lys Gly Ile Arg Lys Ser Ile Cys Ile Glu Ile Asn Asn Gly  
420 425 430

Glu Leu Phe Phe Val Ala Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile  
435 440 445

Asn Thr Pro Lys Glu Ile Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr  
450 455 460

Glu Asn Asp Leu Asp Gln Val Ile Leu Asn Phe Asn Ser Glu Ser Ala  
465 470 475 480

Pro Gly Leu Ser Asp Glu Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala  
485 490 495

Tyr Ile Pro Lys Tyr Asp Ser Asn Gly Thr Ser Asp Ile Glu Gln His  
500 505 510

Asp Val Asn Glu Leu Asn Val Phe Phe Tyr Leu Asp Ala Gln Lys Val  
515 520 525

Pro Glu Gly Glu Asn Asn Val Asn Leu Thr Ser Ser Ile Asp Thr Ala  
530 535 540

Leu Leu Glu Gln Pro Lys Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile  
545 550 555 560

Asn Asn Val Asn Lys Pro Val Gln Ala Ala Leu Phe Val Ser Trp Ile  
565 570 575

Gln Gln Val Leu Val Asp Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr  
580 585 590

Val Asp Lys Ile Ala Asp Ile Ser Ile Val Val Pro Tyr Ile Gly Leu  
595 600 605

Ala Leu Asn Ile Gly Asn Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala  
610 615 620

Leu Glu Leu Leu Gly Ala Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu  
625 630 635 640

Leu Ile Pro Thr Ile Leu Val Phe Thr Ile Lys Ser Phe Leu Gly Ser  
645 650 655

Ser Asp Asn Lys Asn Lys Val Ile Lys Ala Ile Asn Asn Ala Leu Lys  
660 665 670

Glu Arg Asp Glu Lys Trp Lys Glu Val Tyr Ser Phe Ile Val Ser Asn  
675 680 685

Trp Met Thr Lys Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met  
690 695 700

Tyr Gln Ala Leu Gln Asn Gln Val Asn Ala Leu Lys Ala Ile Ile Glu  
705 710 715 720

Ser Lys Tyr Asn Ser Tyr Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn  
725 730 735

Lys Tyr Asp Ile Glu Gln Ile Glu Asn Glu Leu Asn Gln Lys Val Ser  
740 745 750

Ile Ala Met Asn Asn Ile Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser  
755 760 765

Tyr Leu Met Lys Leu Ile Asn Glu Val Lys Ile Asn Lys Leu Arg Glu  
770 775 780

Tyr Asp Glu Asn Val Lys Thr Tyr Leu Leu Asp Tyr Ile Ile Lys His  
785 790 795 800

Gly Ser Ile Leu Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Ile  
805 810 815

Asp Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp  
820 825 830

Asp Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys  
835 840 845

Ser Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp  
850 855 860

Thr Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys  
865 870 875 880

Tyr Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser  
885 890 895

Glu Val Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr  
900 905 910

Lys Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn  
915 920 925

Lys Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg  
930 935 940

Asp Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile  
945 950 955 960

Trp Thr Leu Gln Asp Asn Ser Gly Ile Asn Gln Lys Leu Ala Phe Asn  
965 970 975

Tyr Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe  
980 985 990

Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn  
995 1000 1005

Gly Asn Leu Ile Asp Lys Lys Ser Ile Leu Asn Leu Gly Asn Ile His  
1010 1015 1020

Val Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg  
1025 1030 1035 1040

Tyr Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu  
1045 1050 1055

Thr Glu Ile Gln Thr Leu Tyr Asn Asn Glu Pro Asn Ala Asn Ile Leu  
1060 1065 1070

Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu  
1075 1080 1085

Leu Asn Val Leu Lys Pro Asn Asn Phe Ile Asn Arg Arg Thr Asp Ser  
1090 1095 1100

Thr Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg  
1105 1110 1115 1120

Leu Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser  
1125 1130 1135

Thr Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe  
1140 1145 1150

Val Ala Ser Lys Thr His Leu Leu Pro Leu Tyr Ala Asp Thr Ala Thr  
1155 1160 1165

Thr Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe  
1170 1175 1180

Asn Gln Val Val Val Met Asn Ser Val Gly Cys Thr Met Asn Phe Lys  
1185 1190 1195 1200

Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp Thr  
1205 1210 1215

Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp Asn Thr Asn  
1220 1225 1230

Ser Asn Gly Phe Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp Gln  
1235 1240 1245

Glu Lys  
1250

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3759 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

ATG CCA AAA ATT AAT AGT TTT AAT TAT AAT GAT CCT GTT AAT GAT AGA	48
Met Pro Lys Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Asn Asp Arg	
1 5 10 15	
ACA ATT TTA TAT ATT AAA CCA GGC GGT TGT CAA GAA TTT TAT AAA TCA	96
Thr Ile Leu Tyr Ile Lys Pro Gly Gly Cys Gln Glu Phe Tyr Lys Ser	
20 25 30	
TTT AAT ATT ATG AAA AAT ATT TGG ATA ATT CCA GAG AGA AAT GTA ATT	144
Phe Asn Ile Met Lys Asn Ile Trp Ile Ile Pro Glu Arg Asn Val Ile	
35 40 45	
GGT ACA ACC CCC CAA GAT TTT CAT CCG CCT ACT TCA TTA AAA AAT GGA	192
Gly Thr Thr Pro Gln Asp Phe His Pro Pro Thr Ser Leu Lys Asn Gly	
50 55 60	
GAT AGT AGT TAT TAT GAC CCT AAT TAT TTA CAA AGT GAT GAA GAA AAG	240
Asp Ser Ser Tyr Tyr Asp Pro Asn Tyr Leu Gln Ser Asp Glu Glu Lys	
65 70 75 80	
GAT AGA TTT TTA AAA ATA GTC ACA AAA ATA TTT AAT AGA ATA AAT AAT	288
Asp Arg Phe Leu Lys Ile Val Thr Lys Ile Phe Asn Arg Ile Asn Asn	
85 90 95	
AAT CTT TCA GGA GGG ATT TTA TTA GAA GAA CTG TCA AAA GCT AAT CCA	336
Asn Leu Ser Gly Gly Ile Leu Leu Glu Glu Leu Ser Lys Ala Asn Pro	
100 105 110	
TAT TTA GGG AAT GAT AAT ACT CCA GAT AAT CAA TTC CAT ATT GGT GAT	384
Tyr Leu Gly Asn Asp Asn Thr Pro Asp Asn Gln Phe His Ile Gly Asp	
115 120 125	

GCA TCA GCA GTT GAG ATT AAA TTC TCA AAT GGT AGC CAA GAC ATA CTA Ala Ser Ala Val Glu Ile Lys Phe Ser Asn Gly Ser Gln Asp Ile Leu 130 135 140	432
TTA CCT AAT GTT ATT ATA ATG GGA GCA GAG CCT GAT TTA TTT GAA ACT Leu Pro Asn Val Ile Ile Met Gly Ala Glu Pro Asp Leu Phe Glu Thr 145 150 155 160	480
AAC AGT TCC AAT ATT TCT CTA AGA AAT AAT TAT ATG CCA AGC AAT CAC Asn Ser Ser Asn Ile Ser Leu Arg Asn Asn Tyr Met Pro Ser Asn His 165 170 175	528
GGT TTT GGA TCA ATA GCT ATA GTA ACA TTC TCA CCT GAA TAT TCT TTT Gly Phe Gly Ser Ile Ala Ile Val Thr Phe Ser Pro Glu Tyr Ser Phe 180 185 190	576
AGA TTT AAT GAT AAT AGT ATG AAT GAA TTT ATT CAA GAT CCT GCT CTT Arg Phe Asn Asp Asn Ser Met Asn Glu Phe Ile Gln Asp Pro Ala Leu 195 200 205	624
ACA TTA ATG CAT GAA TTA ATA CAT TCA TTA CAT GGA CTA TAT GGG GCT Thr Leu Met His Glu Leu Ile His Ser Leu His Gly Leu Tyr Gly Ala 210 215 220	672
AAA GGG ATT ACT ACA AAG TAT ACT ATA ACA CAA AAA CAA AAT CCC CTA Lys Gly Ile Thr Thr Lys Tyr Thr Ile Thr Gln Lys Gln Asn Pro Leu 225 230 235 240	720
ATA ACA AAT ATA AGA GGT ACA AAT ATT GAA GAA TTC TTA ACT TTT GGA Ile Thr Asn Ile Arg Gly Thr Asn Ile Glu Glu Phe Leu Thr Phe Gly 245 250 255	768
GGT ACT GAT TTA AAC ATT ATT ACT AGT GCT CAG TCC AAT GAT ATC TAT Gly Thr Asp Leu Asn Ile Ile Thr Ser Ala Gln Ser Asn Asp Ile Tyr 260 265 270	816
ACT AAT CTT CTA GCT GAT TAT AAA AAA ATA GCG TCT AAA CTT AGC AAA Thr Asn Leu Leu Ala Asp Tyr Lys Lys Ile Ala Ser Lys Leu Ser Lys 275 280 285	864
GTA CAA GTA TCT AAT CCA CTA CTT AAT CCT TAT AAA GAT GTT TTT GAA Val Gln Val Ser Asn Pro Leu Leu Asn Pro Tyr Lys Asp Val Phe Glu 290 295 300	912
GCA AAG TAT GGA TTA GAT AAA GAT GCT AGC GGA ATT TAT TCG GTA AAT Ala Lys Tyr Gly Leu Asp Lys Asp Ala Ser Gly Ile Tyr Ser Val Asn 305 310 315 320	960
ATA AAC AAA TTT AAT GAT ATT TTT AAA AAA TTA TAC AGC TTT ACG GAA Ile Asn Lys Phe Asn Asp Ile Phe Lys Lys Leu Tyr Ser Phe Thr Glu 325 330 335	1008
TTT GAT TTA GCA ACT AAA TTT CAA GTT AAA TGT AGG CAA ACT TAT ATT Phe Asp Leu Ala Thr Lys Phe Gln Val Lys Cys Arg Gln Thr Tyr Ile 340 345 350	1056
GGA CAG TAT AAA TAC TTC AAA CTT TCA AAC TTG TTA AAT GAT TCT ATT Gly Gln Tyr Lys Tyr Phe Lys Leu Ser Asn Leu Leu Asn Asp Ser Ile 355 360 365	1104

TAT AAT ATA TCA GAA GGC TAT AAT ATA AAT AAT TTA AAG GTA AAT TTT Tyr Asn Ile Ser Glu Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe 370 375 380	1152
AGA GGA CAG AAT GCA AAT TTA AAT CCT AGA ATT ATT ACA CCA ATT ACA Arg Gly Gln Asn Ala Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Thr 385 390 395 400	1200
GGT AGA GGA CTA GTA AAA AAA ATC ATT AGA TTT TGT AAA AAT ATT GTT Gly Arg Gly Leu Val Lys Lys Ile Ile Arg Phe Cys Lys Asn Ile Val 405 410 415	1248
TCT GTA AAA GGC ATA AGG AAA TCA ATA TGT ATC GAA ATA AAT AAT GGT Ser Val Lys Gly Ile Arg Lys Ser Ile Cys Ile Glu Ile Asn Asn Gly 420 425 430	1296
GAG TTA TTT GTG GCT TCC GAG AAT AGT TAT AAT GAT GAT AAT ATA Glu Leu Phe Phe Val Ala Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile 435 440 445	1344
AAT ACT CCT AAA GAA ATT GAC GAT ACA GTA ACT TCA AAT AAT AAT TAT Asn Thr Pro Lys Glu Ile Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr 450 455 460	1392
GAA AAT GAT TTA GAT CAG GTT ATT TTA AAT TTT AAT AGT GAA TCA GCA Glu Asn Asp Leu Asp Gln Val Ile Leu Asn Phe Asn Ser Glu Ser Ala 465 470 475 480	1440
CCT GGA CTT TCA GAT GAA AAA TTA AAT TTA ACT ATC CAA AAT GAT GCT Pro Gly Leu Ser Asp Glu Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala 485 490 495	1488
TAT ATA CCA AAA TAT GAT TCT AAT GGA ACA AGT GAT ATA GAA CAA CAT Tyr Ile Pro Lys Tyr Asp Ser Asn Gly Thr Ser Asp Ile Glu Gln His 500 505 510	1536
GAT GTT AAT GAA CTT AAT GTA TTT TTC TAT TTA GAT GCA CAG AAA GTG Asp Val Asn Glu Leu Asn Val Phe Phe Tyr Leu Asp Ala Gln Lys Val 515 520 525	1584
CCC GAA GGT GAA AAT AAT GTC AAT CTC ACC TCT TCA ATT GAT ACA GCA Pro Glu Gly Glu Asn Asn Val Asn Leu Thr Ser Ser Ile Asp Thr Ala 530 535 540	1632
TTA TTA GAA CAA CCT AAA ATA TAT ACA TTT TTT TCA TCA GAA TTT ATT Leu Leu Glu Gln Pro Lys Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile 545 550 555 560	1680
AAT AAT GTC AAT AAA CCT GTG CAA GCA GCA TTA TTT GTA AGC TGG ATA Asn Asn Val Asn Lys Pro Val Gln Ala Ala Leu Phe Val Ser Trp Ile 565 570 575	1728
CAA CAA GTG TTA GTA GAT TTT ACT ACT GAA GCT AAC CAA AAA AGT ACT Gln Gln Val Leu Val Asp Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr 580 585 590	1776
GTT GAT AAA ATT GCA GAT ATT TCT ATA GTT GTT CCA TAT ATA GGT CTT Val Asp Lys Ile Ala Asp Ile Ser Ile Val Val Pro Tyr Ile Gly Leu 595 600 605	1824

GCT TTA AAT ATA GGA AAT GAA GCA CAA AAA GGA AAT TTT AAA GAT GCA Ala Leu Asn Ile Gly Asn Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala 610 615 620	1872
CTT GAA TTA TTA GGA GCA GGT ATT TTA TTA GAA TTT GAA CCC GAG CTT Leu Glu Leu Leu Gly Ala Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu 625 630 635 640	1920
TTA ATT CCT ACA ATT TTA GTA TTC ACG ATA AAA TCT TTT TTA GGT TCA Leu Ile Pro Thr Ile Leu Val Phe Thr Ile Lys Ser Phe Leu Gly Ser 645 650 655	1968
TCT GAT AAT AAA AAT AAA GTT ATT AAA GCA ATA AAT AAT GCA TTG AAA Ser Asp Asn Lys Asn Lys Val Ile Lys Ala Ile Asn Asn Ala Leu Lys 660 665 670	2016
GAA AGA GAT GAA AAA TGG AAA GAA GTA TAT AGT TTT ATA GTA TCG AAT Glu Arg Asp Glu Lys Trp Lys Glu Val Tyr Ser Phe Ile Val Ser Asn 675 680 685	2064
TGG ATG ACT AAA ATT AAT ACA CAA TTT AAT AAA AGA AAA GAA CAA ATG Trp Met Thr Lys Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met 690 695 700	2112
TAT CAA GCT TTA CAA AAT CAA GTA AAT GCA ATT AAA ACA ATA ATA GAA Tyr Gln Ala Leu Gln Asn Gln Val Asn Ala Ile Lys Thr Ile Ile Glu 705 710 715 720	2160
TCT AAG TAT AAT AGT TAT ACT TTA GAG GAA AAA AAT GAG CTT ACA AAT Ser Lys Tyr Asn Ser Tyr Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn 725 730 735	2208
AAA TAT GAT ATT AAG CAA ATA GAA AAT GAA CTT AAT CAA AAG GTT TCT Lys Tyr Asp Ile Lys Gln Ile Glu Asn Glu Leu Asn Gln Lys Val Ser 740 745 750	2256
ATA GCA ATG AAT AAT ATA GAC AGG TTC TTA ACT GAA AGT TCT ATA TCC Ile Ala Met Asn Asn Ile Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser 755 760 765	2304
TAT TTA ATG AAA TTA ATA AAT GAA GTA AAA ATT AAT AAA TTA AGA GAA Tyr Leu Met Lys Leu Ile Asn Glu Val Lys Ile Asn Lys Leu Arg Glu 770 775 780	2352
TAT GAT GAG AAT GTC AAA ACG TAT TTA TTG AAT TAT ATT ATA CAA CAT Tyr Asp Glu Asn Val Lys Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His 785 790 795 800	2400
GGA TCA ATC TTG GGA GAG AGT CAG CAA GAA CTA AAT TCT ATG GTA ACT Gly Ser Ile Leu Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr 805 810 815	2448
GAT ACC CTA AAT AAT AGT ATT CCT TTT AAG CTT TCT TCT TAT ACA GAT Asp Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp 820 825 830	2496
GAT AAA ATT TTA ATT TCA TAT TTT AAT AAA TTC TTT AAG AGA ATT AAA Asp Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys 835 840 845	2544

AGT AGT TCA GTT TTA AAT ATG AGA TAT AAA AAT GAT AAA TAC GTA GAT Ser Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp 850 855 860	2592
ACT TCA GGA TAT GAT TCA AAT ATA AAT ATT AAT GGA GAT GTA TAT AAA Thr Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys 865 870 875 880	2640
TAT CCA ACT AAT AAA AAT CAA TTT GGA ATA TAT AAT GAT AAA CTT AGT Tyr Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser 885 890 895	2688
GAA GTT AAT ATA TCT CAA AAT GAT TAC ATT ATA TAT GAT AAT AAA TAT Glu Val Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr 900 905 910	2736
AAA AAT TTT AGT ATT AGT TTT TGG GTA AGA ATT CCT AAC TAT GAT AAT Lys Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn 915 920 925	2784
AAG ATA GTA AAT GTT AAT AAT GAA TAC ACT ATA ATA AAT TGT ATG AGA Lys Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg 930 935 940	2832
GAT AAT AAT TCA GGA TGG AAA GTA TCT CTT AAT CAT AAT GAA ATA ATT Asp Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile 945 950 955 960	2880
TGG ACA TTG CAA GAT AAT GCA GGA ATT AAT CAA AAA TTA GCA TTT AAC Trp Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn 965 970 975	2928
TAT GGT AAC GCA AAT GGT ATT TCT GAT TAT ATA AAT AAG TGG ATT TTT Tyr Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe 980 985 990	2976
GTA ACT ATA ACT AAT GAT AGA TTA GGA GAT TCT AAA CTT TAT ATT AAT Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn 995 1000 1005	3024
GGA AAT TTA ATA GAT CAA AAA TCA ATT TTA AAT TTA GGT AAT ATT CAT Gly Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His 1010 1015 1020	3072
GTT AGT GAC AAT ATA TTA TTT AAA ATA GTT AAT TGT AGT TAT ACA AGA Val Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg 1025 1030 1035 1040	3120
TAT ATT GGT ATT AGA TAT TTT AAT ATT TTT GAT AAA GAA TTA GAT GAA Tyr Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu 1045 1050 1055	3168
ACA GAA ATT CAA ACT TTA TAT AGC AAT GAA CCT AAT ACA AAT ATT TTG Thr Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu 1060 1065 1070	3216
AAG GAT TTT TGG GGA AAT TAT TTG CTT TAT GAC AAA GAA TAC TAT TTA Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu 1075 1080 1085	3264

TTA AAT GTG TTA AAA CCA AAT AAC TTT ATT GAT AGG AGA AAA GAT TCT Leu Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser 1090 1095 1100	3312
ACT TTA AGC ATT AAT ATA AGA AGC ACT ATT CTT TTA GCT AAT AGA Thr Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg 1105 1110 1115 1120	3360
TTA TAT AGT GGA ATA AAA GTT AAA ATA CAA AGA GTT AAT AAT AGT AGT Leu Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser 1125 1130 1135	3408
ACT AAC GAT AAT CTT GTT AGA AAG AAT GAT CAG GTA TAT ATT AAT TTT Thr Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe 1140 1145 1150	3456
GTA GCC AGC AAA ACT CAC TTA TTT CCA TTA TAT GCT GAT ACA GCT ACC Val Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr 1155 1160 1165	3504
ACA AAT AAA GAG AAA ACA ATA AAA ATA TCA TCA TCT GGC AAT AGA TTT Thr Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe 1170 1175 1180	3552
AAT CAA GTA GTA GTT ATG AAT TCA GTA GGA AAT AAT TGT ACA ATG AAT Asn Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn 1185 1190 1195 1200	3600
TTT AAA AAT AAT AAT GGA AAT AAT ATT GGG TTG TTA GGT TTC AAG GCA Phe Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala 1205 1210 1215	3648
GAT ACT GTA GTT GCT AGT ACT TGG TAT TAT ACA CAT ATG AGA GAT CAT Asp Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His 1220 1225 1230	3696
ACA AAC AGC AAT GGA TGT TTT TGG AAC TTT ATT TCT GAA GAA CAT GGA Thr Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly 1235 1240 1245	3744
TGG CAA GAA AAA TAA Trp Gln Glu Lys 1250	3759

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1252 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Pro Lys Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Asn Asp Arg 1 5 10 15
Thr Ile Leu Tyr Ile Lys Pro Gly Gly Cys Gln Glu Phe Tyr Lys Ser 20 25 30

Phe Asn Ile Met Lys Asn Ile Trp Ile Ile Pro Glu Arg Asn Val Ile  
     35                  40                  45  
 Gly Thr Thr Pro Gln Asp Phe His Pro Pro Thr Ser Leu Lys Asn Gly  
     50                  55                  60  
 Asp Ser Ser Tyr Tyr Asp Pro Asn Tyr Leu Gln Ser Asp Glu Glu Lys  
     65                  70                  75                  80  
 Asp Arg Phe Leu Lys Ile Val Thr Lys Ile Phe Asn Arg Ile Asn Asn  
     85                  90                  95  
 Asn Leu Ser Gly Gly Ile Leu Leu Glu Glu Leu Ser Lys Ala Asn Pro  
     100                 105                 110  
 Tyr Leu Gly Asn Asp Asn Thr Pro Asp Asn Gln Phe His Ile Gly Asp  
     115                 120                 125  
 Ala Ser Ala Val Glu Ile Lys Phe Ser Asn Gly Ser Gln Asp Ile Leu  
     130                 135                 140  
 Leu Pro Asn Val Ile Ile Met Gly Ala Glu Pro Asp Leu Phe Glu Thr  
     145                 150                 155                 160  
 Asn Ser Ser Asn Ile Ser Leu Arg Asn Asn Tyr Met Pro Ser Asn His  
     165                 170                 175  
 Gly Phe Gly Ser Ile Ala Ile Val Thr Phe Ser Pro Glu Tyr Ser Phe  
     180                 185                 190  
 Arg Phe Asn Asp Asn Ser Met Asn Glu Phe Ile Gln Asp Pro Ala Leu  
     195                 200                 205  
 Thr Leu Met His Glu Leu Ile His Ser Leu His Gly Leu Tyr Gly Ala  
     210                 215                 220  
 Lys Gly Ile Thr Thr Lys Tyr Thr Ile Thr Gln Lys Gln Asn Pro Leu  
     225                 230                 235                 240  
 Ile Thr Asn Ile Arg Gly Thr Asn Ile Glu Glu Phe Leu Thr Phe Gly  
     245                 250                 255  
 Gly Thr Asp Leu Asn Ile Ile Thr Ser Ala Gln Ser Asn Asp Ile Tyr  
     260                 265                 270  
 Thr Asn Leu Leu Ala Asp Tyr Lys Lys Ile Ala Ser Lys Leu Ser Lys  
     275                 280                 285  
 Val Gln Val Ser Asn Pro Leu Leu Asn Pro Tyr Lys Asp Val Phe Glu  
     290                 295                 300  
 Ala Lys Tyr Gly Leu Asp Lys Asp Ala Ser Gly Ile Tyr Ser Val Asn  
     305                 310                 315                 320  
 Ile Asn Lys Phe Asn Asp Ile Phe Lys Lys Leu Tyr Ser Phe Thr Glu  
     325                 330                 335  
 Phe Asp Leu Ala Thr Lys Phe Gln Val Lys Cys Arg Gln Thr Tyr Ile  
     340                 345                 350  
 Gly Gln Tyr Lys Tyr Phe Lys Leu Ser Asn Leu Leu Asn Asp Ser Ile  
     355                 360                 365

Tyr Asn Ile Ser Glu Gly Tyr Asn Ile Asn Asn Leu Lys Val Asn Phe  
 370 375 380  
 Arg Gly Gln Asn Ala Asn Leu Asn Pro Arg Ile Ile Thr Pro Ile Thr  
 385 390 395 400  
 Gly Arg Gly Leu Val Lys Lys Ile Ile Arg Phe Cys Lys Asn Ile Val  
 405 410 415  
 Ser Val Lys Gly Ile Arg Lys Ser Ile Cys Ile Glu Ile Asn Asn Gly  
 420 425 430  
 Glu Leu Phe Phe Val Ala Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile  
 435 440 445  
 Asn Thr Pro Lys Glu Ile Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr  
 450 455 460  
 Glu Asn Asp Leu Asp Gln Val Ile Leu Asn Phe Asn Ser Glu Ser Ala  
 465 470 475 480  
 Pro Gly Leu Ser Asp Glu Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala  
 485 490 495  
 Tyr Ile Pro Lys Tyr Asp Ser Asn Gly Thr Ser Asp Ile Glu Gln His  
 500 505 510  
 Asp Val Asn Glu Leu Asn Val Phe Phe Tyr Leu Asp Ala Gln Lys Val  
 515 520 525  
 Pro Glu Gly Glu Asn Asn Val Asn Leu Thr Ser Ser Ile Asp Thr Ala  
 530 535 540  
 Leu Leu Glu Gln Pro Lys Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile  
 545 550 555 560  
 Asn Asn Val Asn Lys Pro Val Gln Ala Ala Leu Phe Val Ser Trp Ile  
 565 570 575  
 Gln Gln Val Leu Val Asp Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr  
 580 585 590  
 Val Asp Lys Ile Ala Asp Ile Ser Ile Val Val Pro Tyr Ile Gly Leu  
 595 600 605  
 Ala Leu Asn Ile Gly Asn Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala  
 610 615 620  
 Leu Glu Leu Leu Gly Ala Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu  
 625 630 635 640  
 Leu Ile Pro Thr Ile Leu Val Phe Thr Ile Lys Ser Phe Leu Gly Ser  
 645 650 655  
 Ser Asp Asn Lys Asn Lys Val Ile Lys Ala Ile Asn Asn Ala Leu Lys  
 660 665 670  
 Glu Arg Asp Glu Lys Trp Lys Glu Val Tyr Ser Phe Ile Val Ser Asn  
 675 680 685  
 Trp Met Thr Lys Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met  
 690 695 700

Tyr Gln Ala Leu Gln Asn Gln Val Asn Ala Ile Lys Thr Ile Ile Glu  
705 710 715 720

Ser Lys Tyr Asn Ser Tyr Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn  
725 730 735

Lys Tyr Asp Ile Lys Gln Ile Glu Asn Glu Leu Asn Gln Lys Val Ser  
740 745 750

Ile Ala Met Asn Asn Ile Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser  
755 760 765

Tyr Leu Met Lys Leu Ile Asn Glu Val Lys Ile Asn Lys Leu Arg Glu  
770 775 780

Tyr Asp Glu Asn Val Lys Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His  
785 790 795 800

Gly Ser Ile Leu Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr  
805 810 815

Asp Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp  
820 825 830

Asp Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys  
835 840 845

Ser Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp  
850 855 860

Thr Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys  
865 870 875 880

Tyr Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser  
885 890 895

Glu Val Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr  
900 905 910

Lys Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn  
915 920 925

Lys Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg  
930 935 940

Asp Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile  
945 950 955 960

Trp Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn  
965 970 975

Tyr Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe  
980 985 990

Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn  
995 1000 1005

Gly Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His  
1010 1015 1020

Val Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg  
1025 1030 1035 1040

Tyr Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu  
 1045 1050 1055  
 Thr Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu  
 1060 1065 1070  
 Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu  
 1075 1080 1085  
 Leu Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser  
 1090 1095 1100  
 Thr Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg  
 1105 1110 1115 1120  
 Leu Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser  
 1125 1130 1135  
 Thr Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe  
 1140 1145 1150  
 Val Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr  
 1155 1160 1165  
 Thr Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe  
 1170 1175 1180  
 Asn Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn  
 1185 1190 1195 1200  
 Phe Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala  
 1205 1210 1215  
 Asp Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His  
 1220 1225 1230  
 Thr Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly  
 1235 1240 1245  
 Trp Gln Glu Lys  
 1250

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1463 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 108..1460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AGATCTCGAT CCCGCAGAAAT TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA	60
TTCCCCTCTA GAAATAATT TGTTAACCT TAAGAAGGAG ATATACC ATG GGC CAT Met Gly His	116
1	
CAT CAT CAT CAT CAT CAT CAC AGC AGC GGC CAT ATC GAA GGT His His His His His His Ser Ser Gly His Ile Glu Gly	164
5 10 15	
CGT CAT ATG GCT AGC ATG GCT CTT TCT TAT ACA GAT GAT AAA ATT Arg His Met Ala Ser Met Ala Leu Ser Ser Tyr Thr Asp Asp Lys Ile	212
20 25 30 35	
TTA ATT TCA TAT TTT AAT AAG TTC TTT AAG AGA ATT AAA AGT AGT TCT Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser Ser Ser	260
40 45 50	
GTT TTA AAT ATG AGA TAT AAA AAT GAT AAA TAC GTA GAT ACT TCA GGA Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr Ser Gly	308
55 60 65	
TAT GAT TCA AAT ATA AAT ATT AAT GGA GAT GTA TAT AAA TAT CCA ACT Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr Pro Thr	356
70 75 80	
AAT AAA AAT CAA TTT GGA ATA TAT AAT GAT AAA CTT AGT GAA GTT AAT Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser Glu Val Asn	404
85 90 95	
ATA TCT CAA AAT GAT TAC ATT ATA TAT GAT AAT AAA TAT AAA AAT TTT Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys Asn Phe	452
100 105 110 115	
AGT ATT AGT TTT TGG GTA AGA ATT CCT AAC TAT GAT AAT AAG ATA GTA Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys Ile Val	500
120 125 130	
AAT GTT AAT AAT GAA TAC ACT ATA ATA AAT TGT ATG AGG GAT AAT AAT Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp Asn Asn	548
135 140 145	
TCA GGA TGG AAA GTA TCT CTT AAT CAT AAT GAA ATA ATT TGG ACA TTG Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp Thr Leu	596
150 155 160	
CAA GAT AAT TCA GGA ATT AAT CAA AAA TTA GCA TTT AAC TAT GGT AAC Gln Asp Asn Ser Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr Gly Asn	644
165 170 175	
GCA AAT GGT ATT TCT GAT TAT ATA AAT AAG TGG ATT TTT GTA ACT ATA Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile	692
180 185 190 195	
ACT AAT GAT AGA TTA GGA GAT TCT AAA CTT TAT ATT AAT GGA AAT TTA Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly Asn Leu	740
200 205 210	

ATA GAT AAA AAA TCA ATT TTA AAT TTA GGT AAT ATT CAT GTT AGT GAC Ile Asp Lys Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val Ser Asp 215	220	225	788
AAT ATA TTA TTT AAA ATA GTT AAT TGT AGT TAT ACA AGA TAT ATT GGT Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr Ile Gly 230	235	240	836
ATT AGA TAT TTT AAT ATT TTT GAT AAA GAA TTA GAT GAA ACA GAA ATT Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr Glu Ile 245	250	255	884
CAA ACT TTA TAT AAC AAT GAA CCT AAT GCA AAT ATT TTA AAG GAT TTT Gln Thr Leu Tyr Asn Asn Glu Pro Asn Ala Asn Ile Leu Lys Asp Phe 260	265	270	932
TGG GGA AAT TAT TTG CTT TAT GAC AAA GAA TAC TAT TTA TTA AAT GTG Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu Asn Val 280	285	290	980
TTA AAA CCA AAT AAC TTT ATT AAT AGG AGA ACA GAT TCT ACT TTA AGC Leu Lys Pro Asn Asn Phe Ile Asn Arg Arg Thr Asp Ser Thr Leu Ser 295	300	305	1028
ATT AAT AAT ATA AGA AGC ACT ATT CTT TTA GCT AAT AGA TTA TAT AGT Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu Tyr Ser 310	315	320	1076
GGA ATA AAA GTT AAA ATA CAA AGA GTT AAT AAT AGT AGT ACT AAC GAT Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr Asn Asp 325	330	335	1124
AAT CTT GTT AGA AAG AAT GAT CAG GTA TAT ATT AAT TTT GTA GCC AGC Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val Ala Ser 340	345	350	1172
AAA ACT CAC TTA CTT CCA TTA TAT GCT GAT ACA GCT ACC ACA AAT AAA Lys Thr His Leu Leu Pro Leu Tyr Ala Asp Thr Ala Thr Thr Asn Lys 360	365	370	1220
GAG AAA ACA ATA AAA ATA TCA TCA TCT GGC AAT AGA TTT AAT CAA GTA Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn Gln Val 375	380	385	1268
GTA GTT ATG AAT TCA GTA GGA AAT TGT ACA ATG AAT TTT AAA AAT AAT Val Val Met Asn Ser Val Gly Asn Cys Thr Met Asn Phe Lys Asn Asn 390	395	400	1316
AAT GGA AAT AAT ATT GGG TTG TTA GGT TTC AAG GCA GAT ACT GTA GTT Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp Thr Val Val 405	410	415	1364
GCT AGT ACT TGG TAT TAT ACA CAT ATG AGA GAT AAT ACA AAC AGC AAT Ala Ser Thr Trp Tyr Tyr His Met Arg Asp Asn Thr Asn Ser Asn 420	425	430	1412
GGA TTT TTT TGG AAC TTT ATT TCT GAA GAA CAT GGA TGG CAA GAA AAA Gly Phe Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp Gln Glu Lys 440	445	450	1460
TAA			1463

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Gly His His His His His His His His Ser Ser Gly His  
1 5 10 15

Ile Glu Gly Arg His Met Ala Ser Met Ala Leu Ser Ser Tyr Thr Asp  
20 25 30

Asp Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys  
35 40 45

Ser Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp  
50 55 60

Thr Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys  
65 70 75 80

Tyr Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser  
85 90 95

Glu Val Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr  
100 105 110

Lys Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn  
115 120 125

Lys Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg  
130 135 140

Asp Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile  
145 150 155 160

Trp Thr Leu Gln Asp Asn Ser Gly Ile Asn Gln Lys Leu Ala Phe Asn  
165 170 175

Tyr Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe  
180 185 190

Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn  
195 200 205

Gly Asn Leu Ile Asp Lys Lys Ser Ile Leu Asn Leu Gly Asn Ile His  
210 215 220

Val Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg  
225 230 235 240

Tyr Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu  
245 250 255

Thr Glu Ile Gln Thr Leu Tyr Asn Asn Glu Pro Asn Ala Asn Ile Leu  
260 265 270

Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu  
 275 280 285  
 Leu Asn Val Leu Lys Pro Asn Asn Phe Ile Asn Arg Arg Thr Asp Ser  
 290 295 300  
 Thr Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg  
 305 310 315 320  
 Leu Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser  
 325 330 335  
 Thr Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe  
 340 345 350  
 Val Ala Ser Lys Thr His Leu Leu Pro Leu Tyr Ala Asp Thr Ala Thr  
 355 360 365  
 Thr Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe  
 370 375 380  
 Asn Gln Val Val Val Met Asn Ser Val Gly Asn Cys Thr Met Asn Phe  
 385 390 395 400  
 Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp  
 405 410 415  
 Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp Asn Thr  
 420 425 430  
 Asn Ser Asn Gly Phe Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp  
 435 440 445  
 Gln Glu Lys  
 450

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1472 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 108..1463
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AGATCTCGAT CCCGCATAAT TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA	60
TTCCCCCTCTA GAAATAATTT TGTTTAACCT TAAGAAGGAG ATATACC ATG GGC CAT	116
Met Gly His	
1	
CAT CAT CAT CAT CAT CAT CAC AGC AGC GGC CAT ATC GAA GGT	164
His His His His His His Ser Ser Gly His Ile Glu Gly	
5 10 15	

CGT CAT ATG GCT AGC ATG GCT CTT TCT TAT ACA GAT GAT AAA ATT Arg His Met Ala Ser Met Ala Leu Ser Ser Tyr Thr Asp Asp Lys Ile 20 25 30 35	212
TTA ATT TCA TAT TTT AAT AAA TTC TTT AAG AGA ATT AAA AGT AGT TCA Leu Ile Ser Tyr Phe Asn Lys Phe Lys Arg Ile Lys Ser Ser Ser 40 45 50	260
GTT TTA AAT ATG AGA TAT AAA AAT GAT AAA TAC GTA GAT ACT TCA GGA Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr Ser Gly 55 60 65	308
TAT GAT TCA AAT ATA AAT ATT AAT GGA GAT GTA TAT AAA TAT CCA ACT Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr Pro Thr 70 75 80	356
AAT AAA AAT CAA TTT GGA ATA TAT GAT AAA CTT AGT GAA GTT AAT Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser Glu Val Asn 85 90 95	404
ATA TCT CAA AAT GAT TAC ATT ATA TAT GAT AAT AAA TAT AAA AAT TTT Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys Asn Phe 100 105 110 115	452
AGT ATT AGT TTT TGG GTA AGA ATT CCT AAC TAT GAT AAT AAG ATA GTA Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys Ile Val 120 125 130	500
AAT GTT AAT AAT GAA TAC ACT ATA ATA AAT TGT ATG AGA GAT AAT AAT Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp Asn Asn 135 140 145	548
TCA GGA TGG AAA GTA TCT CTT AAT CAT AAT GAA ATA ATT TGG ACA TTG Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp Thr Leu 150 155 160	596
CAA GAT AAT GCA GGA ATT AAT CAA AAA TTA GCA TTT AAC TAT GGT AAC Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr Gly Asn 165 170 175	644
GCA AAT GGT ATT TCT GAT TAT ATA AAT AAG TGG ATT TTT GTA ACT ATA Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile 180 185 190 195	692
ACT AAT GAT AGA TTA GGA GAT TCT AAA CTT TAT ATT AAT GGA AAT TTA Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly Asn Leu 200 205 210	740
ATA GAT CAA AAA TCA ATT TTA AAT TTA GGT AAT ATT CAT GTT AGT GAC Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val Ser Asp 215 220 225	788
AAT ATA TTA TTT AAA ATA GTT AAT TGT AGT TAT ACA AGA TAT ATT GGT Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr Ile Gly 230 235 240	836
ATT AGA TAT TTT AAT ATT TTT GAT AAA GAA TTA GAT GAA ACA GAA ATT Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr Glu Ile 245 250 255	884

CAA ACT TTA TAT AGC AAT GAA CCT AAT ACA AAT ATT TTG AAG GAT TTT Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys Asp Phe 260                   265                   270                   275	932
TGG GGA AAT TAT TTG CTT TAT GAC AAA GAA TAC TAT TTA TTA AAT GTG Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu Asn Val 280                   285                   290	980
TTA AAA CCA AAT AAC TTT ATT GAT AGG AGA AAA GAT TCT ACT TTA AGC Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr Leu Ser 295                   300                   305	1028
ATT AAT AAT ATA AGA AGC ACT ATT CTT TTA GCT AAT AGA TTA TAT AGT Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu Tyr Ser 310                   315                   320	1076
GGA ATA AAA GTT AAA ATA CAA AGA GTT AAT AAT AGT AGT ACT AAC GAT Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr Asn Asp 325                   330                   335	1124
AAT CTT GTT AGA AAG AAT GAT CAG GTA TAT ATT AAT TTT GTA GCC AGC Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val Ala Ser 340                   345                   350                   355	1172
AAA ACT CAC TTA TTT CCA TTA TAT GCT GAT ACA GCT ACC ACA AAT AAA Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr Asn Lys 360                   365                   370	1220
GAG AAA ACA ATA AAA ATA TCA TCA TCT GGC AAT AGA TTT AAT CAA GTA Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn Gln Val 375                   380                   385	1268
GTA GTT ATG AAT TCA GTA GGA AAT AAT TGT ACA ATG AAT TTT AAA AAT Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe Lys Asn 390                   395                   400	1316
AAT AAT GGA AAT AAT ATT GGG TTG TTA GGT TTC AAG GCA GAT ACT GTA Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp Thr Val 405                   410                   415	1364
GTT GCT AGT ACT TGG TAT TAT ACA CAT ATG AGA GAT CAT ACA AAC AGC Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr Asn Ser 420                   425                   430                   435	1412
AAT GGA TGT TTT TGG AAC TTT ATT TCT GAA GAA CAT GGA TGG CAA GAA Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp Gln Glu 440                   445                   450	1460
<b>AAA TAAAAAGCTT</b> Lys	<b>1472</b>

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 452 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Gly His His His His His His His His Ser Ser Gly His  
1 5 10 15

Ile Glu Gly Arg His Met Ala Ser Met Ala Leu Ser Ser Tyr Thr Asp  
20 25 30

Asp Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys  
35 40 45

Ser Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp  
50 55 60

Thr Ser Gly Tyr Asp Ser Asn Ile Asn Ile Gly Asp Val Tyr Lys  
65 70 75 80

Tyr Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser  
85 90 95

Glu Val Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr  
100 105 110

Lys Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn  
115 120 125

Lys Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg  
130 135 140

Asp Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile  
145 150 155 160

Trp Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn  
165 170 175

Tyr Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe  
180 185 190

Val Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn  
195 200 205

Gly Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His  
210 215 220

Val Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg  
225 230 235 240

Tyr Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu  
245 250 255

Thr Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu  
260 265 270

Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu  
275 280 285

Leu Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser  
290 295 300

Thr Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg  
305 310 315 320

Leu Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser  
 325 330 335  
 Thr Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe  
 340 345 350  
 Val Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr  
 355 360 365  
 Thr Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe  
 370 375 380  
 Asn Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn  
 385 390 395 400  
 Phe Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala  
 405 410 415  
 Asp Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His  
 420 425 430  
 Thr Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly  
 435 440 445  
 Trp Gln Glu Lys  
 450

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CGCCATGGCT CTTTCTTCTT ATACAGATGA T

31

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GCAAGCTTTT ATTTTCTTG CCATCCATG

29

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ATG CCA ATA ACA ATT AAC AAC TTT AAT TAT TCA GAT CCT GTT GAT AAT Met Pro Ile Thr Ile Asn Asn Phe Asn Tyr Ser Asp Pro Val Asp Asn	48
1                   5                   10                   15	
AAA AAT ATT TTA TAT TTA GAT ACT CAT TTA AAT ACA CTA GCT AAT GAG Lys Asn Ile Leu Tyr Leu Asp Thr His Leu Asn Thr Leu Ala Asn Glu	96
20                   25                   30	
CCT GAA AAA GCC TTT CGC ATT ACA GGA AAT ATA TGG GTA ATA CCT GAT Pro Glu Lys Ala Phe Arg Ile Thr Gly Asn Ile Trp Val Ile Pro Asp	144
35                   40                   45	
AGA TTT TCA AGA AAT TCT AAT CCA AAT TTA AAT AAA CCT CCT CGA GTT Arg Phe Ser Arg Asn Ser Asn Pro Asn Leu Asn Lys Pro Pro Arg Val	192
50                   55                   60	
ACA AGC CCT AAA AGT GGT TAT TAT GAT CCT AAT TAT TTG AGT ACT GAT Thr Ser Pro Lys Ser Gly Tyr Tyr Asp Pro Asn Tyr Leu Ser Thr Asp	240
65                   70                   75                   80	
TCT GAC AAA GAT ACA TTT TTA AAA GAA ATT ATA AAG TTA TTT AAA AGA Ser Asp Lys Asp Thr Phe Leu Lys Glu Ile Ile Lys Leu Phe Lys Arg	288
85                   90                   95	
ATT AAT TCT AGA GAA ATA GGA GAA TTA ATA TAT AGA CTT TCG ACA Ile Asn Ser Arg Glu Ile Gly Glu Leu Ile Tyr Arg Leu Ser Thr	336
100                  105                  110	
GAT ATA CCC TTT CCT GGG AAT AAC AAT ACT CCA ATT AAT ACT TTT GAT Asp Ile Pro Phe Pro Gly Asn Asn Asn Thr Pro Ile Asn Thr Phe Asp	384
115                  120                  125	
TTT GAT GTA GAT TTT AAC AGT GTT GAT GTT AAA ACT AGA CAA GGT AAC Phe Asp Val Asp Phe Asn Ser Val Asp Val Lys Thr Arg Gln Gly Asn	432
130                  135                  140	
AAC TGG GTT AAA ACT GGT AGC ATA AAT CCT AGT GTT ATA ATA ACT GGA Asn Trp Val Lys Thr Gly Ser Ile Asn Pro Ser Val Ile Ile Thr Gly	480
145                  150                  155                  160	
CCT AGA GAA AAC ATT ATA GAT CCA GAA ACT TCT ACG TTT AAA TTA ACT Pro Arg Glu Asn Ile Ile Asp Pro Glu Thr Ser Thr Phe Lys Leu Thr	528
165                  170                  175	

AAC AAT ACT TTT GCG GCA CAA GAA GGA TTT GGT GCT TTA TCA ATA ATT Asn Asn Thr Phe Ala Ala Gln Glu Gly Phe Gly Ala Leu Ser Ile Ile 180 185 190	576
TCA ATA TCA CCT AGA TTT ATG CTA ACA TAT AGT AAT GCA ACT AAT GAT Ser Ile Ser Pro Arg Phe Met Leu Thr Tyr Ser Asn Ala Thr Asn Asp 195 200 205	624
GTA GGA GAG GGT AGA TTT TCT AAG TCT GAA TTT TGC ATG GAT CCA ATA Val Gly Glu Gly Arg Phe Ser Lys Ser Glu Phe Cys Met Asp Pro Ile 210 215 220	672
CTA ATT TTA ATG CAT GAA CTT AAT CAT GCA ATG CAT AAT TTA TAT GGA Leu Ile Leu Met His Glu Leu Asn His Ala Met His Asn Leu Tyr Gly 225 230 235 240	720
ATA GCT ATA CCA AAT GAT CAA ACA ATT TCA TCT GTA ACT AGT AAT ATT Ile Ala Ile Pro Asn Asp Gln Thr Ile Ser Ser Val Thr Ser Asn Ile 245 250 255	768
TTT TAT TCT CAA TAT AAT GTG AAA TTA GAG TAT GCA GAA ATA TAT GCA Phe Tyr Ser Gln Tyr Asn Val Lys Leu Glu Tyr Ala Glu Ile Tyr Ala 260 265 270	816
TTT GGA GGT CCA ACT ATA GAC CTT ATT CCT AAA AGT GCA AGG AAA TAT Phe Gly Gly Pro Thr Ile Asp Leu Ile Pro Lys Ser Ala Arg Lys Tyr 275 280 285	864
TTT GAG GAA AAG GCA TTG GAT TAT TAT AGA TCT ATA GCT AAA AGA CTT Phe Glu Glu Lys Ala Leu Asp Tyr Tyr Arg Ser Ile Ala Lys Arg Leu 290 295 300	912
AAT AGT ATA ACT ACT GCA AAT CCT TCA AGC TTT AAT AAA TAT ATA GGG Asn Ser Ile Thr Thr Ala Asn Pro Ser Ser Phe Asn Lys Tyr Ile Gly 305 310 315 320	960
GAA TAT AAA CAG AAA CTT ATT AGA AAG TAT AGA TTC GTA GTA GAA TCT Glu Tyr Lys Gln Lys Leu Ile Arg Lys Tyr Arg Phe Val Val Glu Ser 325 330 335	1008
TCA GGT GAA GTT ACA GTA AAT CGT AAT AAG TTT GTT GAG TTA TAT AAT Ser Gly Glu Val Thr Val Asn Arg Asn Lys Phe Val Glu Leu Tyr Asn 340 345 350	1056
GAA CTT ACA CAA ATA TTT ACA GAA TTT AAC TAC GCT AAA ATA TAT AAT Glu Leu Thr Gln Ile Phe Thr Glu Phe Asn Tyr Ala Lys Ile Tyr Asn 355 360 365	1104
GTA CAA AAT AGG AAA ATA TAT CTT TCA AAT GTA TAT ACT CCG GTT ACG Val Gln Asn Arg Lys Ile Tyr Leu Ser Asn Val Tyr Thr Pro Val Thr 370 375 380	1152
GCG AAT ATA TTA GAC GAT AAT GTT TAT GAT ATA CAA AAT GGA TTT AAT Ala Asn Ile Leu Asp Asp Asn Val Tyr Asp Ile Gln Asn Gly Phe Asn 385 390 395 400	1200
ATA CCT AAA AGT AAT TTA AAT GTA CTA TTT ATG GGT CAA AAT TTA TCT Ile Pro Lys Ser Asn Leu Asn Val Leu Phe Met Gly Gln Asn Leu Ser 405 410 415	1248

CGA AAT CCA GCA TTA AGA AAA GTC AAT CCT GAA AAT ATG CTT TAT TTA Arg Asn Pro Ala Leu Arg Lys Val Asn Pro Glu Asn Met Leu Tyr Leu 420 425 430	1296
TTT ACA AAA TTT TGT CAT AAA GCA ATA GAT GGT AGA TCA TTA TAT AAT Phe Thr Lys Phe Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn 435 440 445	1344
AAA ACA TTA GAT TGT AGA GAG CTT TTA GTT AAA AAT ACT GAC TTA CCC Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys Asn Thr Asp Leu Pro 450 455 460	1392
TTT ATA GGT GAT ATT AGT GAT GTT AAA ACT GAT ATA TTT TTA AGA AAA Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp Ile Phe Leu Arg Lys 465 470 475 480	1440
GAT ATT AAT GAA GAA ACT GAA GTT ATA TAC TAT CCG GAC AAT GTT TCA Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr Pro Asp Asn Val Ser 485 490 495	1488
GTA GAT CAA GTT ATT CTC AGT AAG AAT ACC TCA GAA CAT GGA CAA CTA Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser Glu His Gln Leu 500 505 510	1536
GAT TTA TTA TAC CCT AGT ATT GAC AGT GAG AGT GAA ATA TTA CCA GGG Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser Glu Ile Leu Pro Gly 515 520 525	1584
GAG AAT CAA GTC TTT TAT GAT AAT AGA ACT CAA AAT GTT GAT TAT TTG Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln Asn Val Asp Tyr Leu 530 535 540	1632
AAT TCT TAT TAT TAC CTA GAA TCT CAA AAA CTA AGT GAT AAT GTT GAA Asn Ser Tyr Tyr Leu Glu Ser Gln Lys Leu Ser Asp Asn Val Glu 545 550 555 560	1680
GAT TTT ACT TTT ACG AGA TCA ATT GAG GAG GCT TTG GAT AAT AGT GCA Asp Phe Thr Phe Arg Ser Ile Glu Glu Ala Leu Asp Asn Ser Ala 565 570 575	1728
AAA GTA TAT ACT TAC TTT CCT ACA CTA GCT AAT AAA GTA AAT GCG GGT Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn Lys Val Asn Ala Gly 580 585 590	1776
GTT CAA GGT GGT TTA TTT TTA ATG TGG GCA AAT GAT GTA GTT GAA GAT Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn Asp Val Val Glu Asp 595 600 605	1824
TTT ACT ACA AAT ATT CTA AGA AAA GAT ACA TTA GAT AAA ATA TCA GAT Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu Asp Lys Ile Ser Asp 610 615 620	1872
GTA TCA GCT ATT ATT CCC TAT ATA GGA CCC GCA TTA AAT ATA AGT AAT Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Ser Asn 625 630 635 640	1920
TCT GTA AGA AGA GGA AAT TTT ACT GAA GCA TTT GCA GTT ACT GGT GTA Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe Ala Val Thr Gly Val 645 650 655	1968

ACT ATT TTA TTA GAA GCA TTT CCT GAA TTT ACA ATA CCT GCA CTT GGT Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr Ile Pro Ala Leu Gly 660 665 670	2016
GCA TTT GTG ATT TAT AGT AAG GTT CAA GAA AGA AAC GAG ATT ATT AAA Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg Asn Glu Ile Ile Lys 675 680 685	2064
ACT ATA GAT AAT TGT TTA GAA CAA AGG ATT AAG AGA TGG AAA GAT TCA Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys Arg Trp Lys Asp Ser 690 695 700	2112
TAT GAA TGG ATG ATG GGA ACG TGG TTA TCC AGG ATT ATT ACT CAA TTT Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg Ile Ile Thr Gln Phe 705 710 715 720	2160
AAT AAT ATA AGT TAT CAA ATG TAT GAT TCT TTA AAT TAT CAG GCA GGT Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu Asn Tyr Gln Ala Gly 725 730 735	2208
GCA ATC AAA GCT AAA ATA GAT TTA GAA TAT AAA AAA TAT TCA GGA AGT Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Tyr Ser Gly Ser 740 745 750	2256
GAT AAA GAA AAT ATA AAA AGT CAA GTT GAA AAT TTA AAA AAT AGT TTA Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu 755 760 765	2304
GAT GTA AAA ATT TCG GAA GCA ATG AAT AAT ATA AAT AAA TTT ATA CGA Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg 770 775 780	2352
GAA TGT TCC GTA ACA TAT TTA TTT AAA AAT ATG TTA CCT AAA GTA ATT Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile 785 790 795 800	2400
GAT GAA TTA AAT GAG TTT GAT CGA AAT ACT AAA GCA AAA TTA ATT AAT Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys Ala Lys Leu Ile Asn 805 810 815	2448
CTT ATA GAT AGT CAT AAT ATT ATT CTA GTT GGT GAA GTA GAT AAA TTA Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu Val Asp Lys Leu 820 825 830	2496
AAA GCA AAA GTA AAT AAT AGC TTT CAA AAT ACA ATA CCC TTT AAT ATT Lys Ala Lys Val Asn Asn Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile 835 840 845	2544
TTT TCA TAT ACT AAT AAT TCT TTA TTA AAA GAT ATA ATT AAT GAA TAT Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr 850 855 860	2592
TTC AAT AAT ATT AAT GAT TCA AAA ATT TTG AGC CTA CAA AAC AGA AAA Phe Asn Asn Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys 865 870 875 880	2640
AAT ACT TTA GTG GAT ACA TCA GGA TAT AAT GCA GAA GTG AGT GAA GAA Asn Thr Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu 885 890 895	2688

GGC GAT GTT CAG CTT AAT CCA ATA TTT CCA TTT GAC TTT AAA TTA GGT Gly Asp Val Gln Leu Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly 900 905 910	2736
AGT TCA GGG GAG GAT AGA GGT AAA GTT ATA GTA ACC CAG AAT GAA AAT Ser Ser Gly Glu Asp Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn 915 920 925	2784
ATT GTA TAT AAT TCT ATG TAT GAA AGT TTT AGC ATT AGT TTT TGG ATT Ile Val Tyr Asn Ser Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile 930 935 940	2832
AGA ATA AAT AAA TGG GTA AGT AAT TTA CCT GGA TAT ACT ATA ATT GAT Arg Ile Asn Lys Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp 945 950 955 960	2880
AGT GTT AAA AAT AAC TCA GGT TGG AGT ATA GGT ATT ATT AGT AAT TTT Ser Val Lys Asn Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe 965 970 975	2928
TTA GTA TTT ACT TTA AAA CAA AAT GAA GAT AGT GAA CAA AGT ATA AAT Leu Val Phe Thr Leu Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn 980 985 990	2976
TTT AGT TAT GAT ATA TCA AAT AAT GCT CCT GGA TAC AAT AAA TGG TTT Phe Ser Tyr Asp Ile Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe 995 1000 1005	3024
TTT GTA ACT GTT ACT AAC AAT ATG ATG GGA AAT ATG AAG ATT TAT ATA Phe Val Thr Val Thr Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile 1010 1015 1020	3072
AAT GGA AAA TTA ATA GAT ACT ATA AAA GTT AAA GAA CTA ACT GGA ATT Asn Gly Lys Leu Ile Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile 1025 1030 1035 1040	3120
AAT TTT AGC AAA ACT ATA ACA TTT GAA ATA AAT AAA ATT CCA GAT ACC Asn Phe Ser Lys Thr Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr 1045 1050 1055	3168
GGT TTG ATT ACT TCA GAT TCT GAT AAC ATC AAT ATG TGG ATA AGA GAT Gly Leu Ile Thr Ser Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp 1060 1065 1070	3216
TTT TAT ATA TTT GCT AAA GAA TTA GAT GGT AAA GAT ATT AAT ATA TTA Phe Tyr Ile Phe Ala Lys Glu Leu Asp Gly Lys Asp Ile Asn Ile Leu 1075 1080 1085	3264
TTT AAT AGC TTG CAA TAT ACT AAT GTT GTA AAA GAT TAT TGG GGA AAT Phe Asn Ser Leu Gln Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn 1090 1095 1100	3312
GAT TTA AGA TAT AAT AAA GAA TAT TAT ATG GTT AAT ATA GAT TAT TTA Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr Met Val Asn Ile Asp Tyr Leu 1105 1110 1115 1120	3360
AAT AGA TAT ATG TAT GCG AAC TCA CGA CAA ATT GTT TTT AAT ACA CGT Asn Arg Tyr Met Tyr Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg 1125 1130 1135	3408

AGA AAT AAT AAT GAC TTC AAT GAA GGA TAT AAA ATT ATA ATA AAA AGA Arg Asn Asn Asn Asp Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg 1140 1145 1150	3456
ATC AGA GGA AAT ACA AAT GAT ACT AGA GTA CGA GGA GGA GAT ATT TTA Ile Arg Gly Asn Thr Asn Asp Thr Arg Val Arg Gly Gly Asp Ile Leu 1155 1160 1165	3504
TAT TTT GAT ATG ACA ATT AAT AAC AAA GCA TAT AAT TTG TTT ATG AAG Tyr Phe Asp Met Thr Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys 1170 1175 1180	3552
AAT GAA ACT ATG TAT GCA GAT AAT CAT AGT ACT GAA GAT ATA TAT GCT Asn Glu Thr Met Tyr Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala 1185 1190 1195 1200	3600
ATA GGT TTA AGA GAA CAA ACA AAG GAT ATA AAT GAT AAT ATT ATA TTT Ile Gly Leu Arg Glu Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe 1205 1210 1215	3648
CAA ATA CAA CCA ATG AAT AAT ACT TAT TAT TAC GCA TCT CAA ATA TTT Gln Ile Gln Pro Met Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe 1220 1225 1230	3696
AAA TCA AAT TTT AAT GGA GAA AAT ATT TCT GGA ATA TGT TCA ATA GGT Lys Ser Asn Phe Asn Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile Gly 1235 1240 1245	3744
ACT TAT CGT TTT AGA CTT GGA GGT GAT TGG TAT AGA CAC AAT TAT TTG Thr Tyr Arg Phe Arg Leu Gly Gly Asp Trp Tyr Arg His Asn Tyr Leu 1250 1255 1260	3792
GTG CCT ACT GTG AAG CAA GGA AAT TAT GCT TCA TTA TTA GAA TCA ACA Val Pro Thr Val Lys Gln Gly Asn Tyr Ala Ser Leu Leu Glu Ser Thr 1265 1270 1275 1280	3840
TCA ACT CAT TGG GGT TTT GTA CCT GTA AGT GAA TAA Ser Thr His Trp Gly Phe Val Pro Val Ser Glu 1285 1290	3876

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1291 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met Pro Ile Thr Ile Asn Asn Phe Asn Tyr Ser Asp Pro Val Asp Asn 1 5 10 15
Lys Asn Ile Leu Tyr Leu Asp Thr His Leu Asn Thr Leu Ala Asn Glu 20 25 30
Pro Glu Lys Ala Phe Arg Ile Thr Gly Asn Ile Trp Val Ile Pro Asp 35 40 45
Arg Phe Ser Arg Asn Ser Asn Pro Asn Leu Asn Lys Pro Pro Arg Val 50 55 60

Thr Ser Pro Lys Ser Gly Tyr Tyr Asp Pro Asn Tyr Leu Ser Thr Asp  
65 70 75 80

Ser Asp Lys Asp Thr Phe Leu Lys Glu Ile Ile Lys Leu Phe Lys Arg  
85 90 95

Ile Asn Ser Arg Glu Ile Gly Glu Leu Ile Tyr Arg Leu Ser Thr  
100 105 110

Asp Ile Pro Phe Pro Gly Asn Asn Asn Thr Pro Ile Asn Thr Phe Asp  
115 120 125

Phe Asp Val Asp Phe Asn Ser Val Asp Val Lys Thr Arg Gln Gly Asn  
130 135 140

Asn Trp Val Lys Thr Gly Ser Ile Asn Pro Ser Val Ile Ile Thr Gly  
145 150 155 160

Pro Arg Glu Asn Ile Ile Asp Pro Glu Thr Ser Thr Phe Lys Leu Thr  
165 170 175

Asn Asn Thr Phe Ala Ala Gln Glu Gly Phe Gly Ala Leu Ser Ile Ile  
180 185 190

Ser Ile Ser Pro Arg Phe Met Leu Thr Tyr Ser Asn Ala Thr Asn Asp  
195 200 205

Val Gly Glu Gly Arg Phe Ser Lys Ser Glu Phe Cys Met Asp Pro Ile  
210 215 220

Leu Ile Leu Met His Glu Leu Asn His Ala Met His Asn Leu Tyr Gly  
225 230 235 240

Ile Ala Ile Pro Asn Asp Gln Thr Ile Ser Ser Val Thr Ser Asn Ile  
245 250 255

Phe Tyr Ser Gln Tyr Asn Val Lys Leu Glu Tyr Ala Glu Ile Tyr Ala  
260 265 270

Phe Gly Gly Pro Thr Ile Asp Leu Ile Pro Lys Ser Ala Arg Lys Tyr  
275 280 285

Phe Glu Glu Lys Ala Leu Asp Tyr Tyr Arg Ser Ile Ala Lys Arg Leu  
290 295 300

Asn Ser Ile Thr Thr Ala Asn Pro Ser Ser Phe Asn Lys Tyr Ile Gly  
305 310 315 320

Glu Tyr Lys Gln Lys Leu Ile Arg Lys Tyr Arg Phe Val Val Glu Ser  
325 330 335

Ser Gly Glu Val Thr Val Asn Arg Asn Lys Phe Val Glu Leu Tyr Asn  
340 345 350

Glu Leu Thr Gln Ile Phe Thr Glu Phe Asn Tyr Ala Lys Ile Tyr Asn  
355 360 365

Val Gln Asn Arg Lys Ile Tyr Leu Ser Asn Val Tyr Thr Pro Val Thr  
370 375 380

Ala Asn Ile Leu Asp Asp Asn Val Tyr Asp Ile Gln Asn Gly Phe Asn  
385 390 395 400

Ile Pro Lys Ser Asn Leu Asn Val Leu Phe Met Gly Gln Asn Leu Ser  
 405 410 415  
 Arg Asn Pro Ala Leu Arg Lys Val Asn Pro Glu Asn Met Leu Tyr Leu  
 420 425 430  
 Phe Thr Lys Phe Cys His Lys Ala Ile Asp Gly Arg Ser Leu Tyr Asn  
 435 440 445  
 Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys Asn Thr Asp Leu Pro  
 450 455 460  
 Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp Ile Phe Leu Arg Lys  
 465 470 475 480  
 Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr Pro Asp Asn Val Ser  
 485 490 495  
 Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser Glu His Gly Gln Leu  
 500 505 510  
 Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser Glu Ile Leu Pro Gly  
 515 520 525  
 Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln Asn Val Asp Tyr Leu  
 530 535 540  
 Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser Asp Asn Val Glu  
 545 550 555 560  
 Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala Leu Asp Asn Ser Ala  
 565 570 575  
 Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn Lys Val Asn Ala Gly  
 580 585 590  
 Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn Asp Val Val Glu Asp  
 595 600 605  
 Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu Asp Lys Ile Ser Asp  
 610 615 620  
 Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Ser Asn  
 625 630 635 640  
 Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe Ala Val Thr Gly Val  
 645 650 655  
 Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr Ile Pro Ala Leu Gly  
 660 665 670  
 Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg Asn Glu Ile Ile Lys  
 675 680 685  
 Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys Arg Trp Lys Asp Ser  
 690 695 700  
 Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg Ile Ile Thr Gln Phe  
 705 710 715 720  
 Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu Asn Tyr Gln Ala Gly  
 725 730 735

Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Tyr Ser Gly Ser  
 740 745 750  
 Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu  
 755 760 765  
 Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg  
 770 775 780  
 Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile  
 785 790 795 800  
 Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys Ala Lys Leu Ile Asn  
 805 810 815  
 Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu Val Asp Lys Leu  
 820 825 830  
 Lys Ala Lys Val Asn Asn Ser Phe Gln Asn Thr Ile Pro Phe Asn Ile  
 835 840 845  
 Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr  
 850 855 860  
 Phe Asn Asn Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys  
 865 870 875 880  
 Asn Thr Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu  
 885 890 895  
 Gly Asp Val Gln Leu Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly  
 900 905 910  
 Ser Ser Gly Glu Asp Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn  
 915 920 925  
 Ile Val Tyr Asn Ser Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile  
 930 935 940  
 Arg Ile Asn Lys Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp  
 945 950 955 960  
 Ser Val Lys Asn Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe  
 965 970 975  
 Leu Val Phe Thr Leu Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn  
 980 985 990  
 Phe Ser Tyr Asp Ile Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe  
 995 1000 1005  
 Phe Val Thr Val Thr Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile  
 1010 1015 1020  
 Asn Gly Lys Leu Ile Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile  
 1025 1030 1035 1040  
 Asn Phe Ser Lys Thr Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr  
 1045 1050 1055  
 Gly Leu Ile Thr Ser Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp  
 1060 1065 1070

Phe Tyr Ile Phe Ala Lys Glu Leu Asp Gly Lys Asp Ile Asn Ile Leu  
 1075 1080 1085  
 Phe Asn Ser Leu Gln Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn  
 1090 1095 1100  
 Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr Met Val Asn Ile Asp Tyr Leu  
 1105 1110 1115 1120  
 Asn Arg Tyr Met Tyr Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg  
 1125 1130 1135  
 Arg Asn Asn Asn Asp Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg  
 1140 1145 1150  
 Ile Arg Gly Asn Thr Asn Asp Thr Arg Val Arg Gly Gly Asp Ile Leu  
 1155 1160 1165  
 Tyr Phe Asp Met Thr Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys  
 1170 1175 1180  
 Asn Glu Thr Met Tyr Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala  
 1185 1190 1195 1200  
 Ile Gly Leu Arg Glu Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe  
 1205 1210 1215  
 Gln Ile Gln Pro Met Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe  
 1220 1225 1230  
 Lys Ser Asn Phe Asn Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile Gly  
 1235 1240 1245  
 Thr Tyr Arg Phe Arg Leu Gly Gly Asp Trp Tyr Arg His Asn Tyr Leu  
 1250 1255 1260  
 Val Pro Thr Val Lys Gln Gly Asn Tyr Ala Ser Leu Leu Glu Ser Thr  
 1265 1270 1275 1280  
 Ser Thr His Trp Gly Phe Val Pro Val Ser Glu  
 1285 1290

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1502 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 108..1493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AGATCTCGAT CCCGCGAAAT TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA	60
TTCCCCCTCTA GAAATAATTT TGTTTAACCTT TAAGAAGGAG ATATACC ATG GGC CAT Met Gly His	116 1
CAT CAT CAT CAT CAT CAT CAC AGC AGC GGC CAT ATC GAA GGT His His His His His His Ser Ser Gly His Ile Glu Gly	164 5               10               15
CGT CAT ATG GCT AGC ATG GCT TTA TTA AAA GAT ATA ATT AAT GAA TAT Arg His Met Ala Ser Met Ala Leu Leu Lys Asp Ile Ile Asn Glu Tyr	212 20              25              30              35
TTC AAT AAT ATT AAT GAT TCA AAA ATT TTG AGC CTA CAA AAC AGA AAA Phe Asn Asn Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Arg Lys	260 40              45              50
AAT ACT TTA GTG GAT ACA TCA GGA TAT AAT GCA GAA GTG AGT GAA GAA Asn Thr Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val Ser Glu Glu	308 55              60              65
GGC GAT GTT CAG CTT AAT CCA ATA TTT CCA TTT GAC TTT AAA TTA GGT Gly Asp Val Gln Leu Asn Pro Ile Phe Pro Phe Asp Phe Lys Leu Gly	356 70              75              80
AGT TCA GGG GAG GAT AGA GGT AAA GTT ATA GTA ACC CAG AAT GAA AAT Ser Ser Gly Glu Asp Arg Gly Lys Val Ile Val Thr Gln Asn Glu Asn	404 85              90              95
ATT GTA TAT AAT TCT ATG TAT GAA AGT TTT AGC ATT AGT TTT TGG ATT Ile Val Tyr Asn Ser Met Tyr Glu Ser Phe Ser Ile Ser Phe Trp Ile	452 100             105             110             115
AGA ATA AAT AAA TGG GTA AGT AAT TTA CCT GGA TAT ACT ATA ATT GAT Arg Ile Asn Lys Trp Val Ser Asn Leu Pro Gly Tyr Thr Ile Ile Asp	500 120             125             130
AGT GTT AAA AAT AAC TCA GGT TGG AGT ATA GGT ATT ATT AGT AAT TTT Ser Val Lys Asn Asn Ser Gly Trp Ser Ile Gly Ile Ile Ser Asn Phe	548 135             140             145
TTA GTA TTT ACT TTA AAA CAA AAT GAA GAT AGT GAA CAA AGT ATA AAT Leu Val Phe Thr Leu Lys Gln Asn Glu Asp Ser Glu Gln Ser Ile Asn	596 150             155             160
TTT AGT TAT GAT ATA TCA AAT AAT GCT CCT GGA TAC AAT AAA TGG TTT Phe Ser Tyr Asp Ile Ser Asn Asn Ala Pro Gly Tyr Asn Lys Trp Phe	644 165             170             175
TTT GTA ACT GTT ACT AAC AAT ATG ATG GGA AAT ATG AAG ATT TAT ATA Phe Val Thr Val Thr Asn Asn Met Met Gly Asn Met Lys Ile Tyr Ile	692 180             185             190             195
AAT GGA AAA TTA ATA GAT ACT ATA AAA GTT AAA GAA CTA ACT GGA ATT Asn Gly Lys Leu Ile Asp Thr Ile Lys Val Lys Glu Leu Thr Gly Ile	740 200             205             210

AAT TTT AGC AAA ACT ATA ACA TTT GAA ATA AAT AAA ATT CCA GAT ACC Asn Phe Ser Lys Thr Ile Thr Phe Glu Ile Asn Lys Ile Pro Asp Thr 215 220 225	788
GGT TTG ATT ACT TCA GAT TCT GAT AAC ATC AAT ATG TGG ATA AGA GAT Gly Leu Ile Thr Ser Asp Ser Asp Asn Ile Asn Met Trp Ile Arg Asp 230 235 240	836
TTT TAT ATA TTT GCT AAA GAA TTA GAT GGT AAA GAT ATT AAT ATA TTA Phe Tyr Ile Phe Ala Lys Glu Leu Asp Gly Lys Asp Ile Asn Ile Leu 245 250 255	884
TTT AAT AGC TTG CAA TAT ACT AAT GTT GTA AAA GAT TAT TGG GGA AAT Phe Asn Ser Leu Gln Tyr Thr Asn Val Val Lys Asp Tyr Trp Gly Asn 260 265 270 275	932
GAT TTA AGA TAT AAT AAA GAA TAT TAT ATG GTT AAT ATA GAT TAT TTA Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr Met Val Asn Ile Asp Tyr Leu 280 285 290	980
AAT AGA TAT ATG TAT GCG AAC TCA CGA CAA ATT GTT TTT AAT ACA CGT Asn Arg Tyr Met Tyr Ala Asn Ser Arg Gln Ile Val Phe Asn Thr Arg 295 300 305	1028
AGA AAT AAT AAT GAC TTC AAT GAA GGA TAT AAA ATT ATA ATA AAA AGA Arg Asn Asn Asn Asp Phe Asn Glu Gly Tyr Lys Ile Ile Ile Lys Arg 310 315 320	1076
ATC AGA GGA AAT ACA AAT GAT ACT AGA GTA CGA GGA GGA GAT ATT TTA Ile Arg Gly Asn Thr Asn Asp Thr Arg Val Arg Gly Gly Asp Ile Leu 325 330 335	1124
TAT TTT GAT ATG ACA ATT AAT AAC AAA GCA TAT AAT TTG TTT ATG AAG Tyr Phe Asp Met Thr Ile Asn Asn Lys Ala Tyr Asn Leu Phe Met Lys 340 345 350 355	1172
AAT GAA ACT ATG TAT GCA GAT AAT CAT AGT ACT GAA GAT ATA TAT GCT Asn Glu Thr Met Tyr Ala Asp Asn His Ser Thr Glu Asp Ile Tyr Ala 360 365 370	1220
ATA GGT TTA AGA GAA CAA ACA AAG GAT ATA AAT GAT AAT ATT ATA TTT Ile Gly Leu Arg Glu Gln Thr Lys Asp Ile Asn Asp Asn Ile Ile Phe 375 380 385	1268
CAA ATA CAA CCA ATG AAT ACT TAT TAT TAC GCA TCT CAA ATA TTT Gln Ile Gln Pro Met Asn Asn Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe 390 395 400	1316
AAA TCA AAT TTT AAT GGA GAA AAT ATT TCT GGA ATA TGT TCA ATA GGT Lys Ser Asn Phe Asn Gly Glu Asn Ile Ser Gly Ile Cys Ser Ile Gly 405 410 415	1364
ACT TAT CGT TTT AGA CTT GGA GGT GAT TGG TAT AGA CAC AAT TAT TTG Thr Tyr Arg Phe Arg Leu Gly Gly Asp Trp Tyr Arg His Asn Tyr Leu 420 425 430 435	1412
GTG CCT ACT GTG AAG CAA GGA AAT TAT GCT TCA TTA TTA GAA TCA ACA Val Pro Thr Val Lys Gln Gly Asn Tyr Ala Ser Leu Leu Glu Ser Thr 440 445 450	1460

TCA ACT CAT TGG GGT TTT GTA CCT GTA AGT GAA TAAAAGCTT  
Ser Thr His Trp Gly Phe Val Pro Val Ser Glu  
455 460

1502

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Gly His His His His His His His His Ser Ser Gly His  
1 5 10 15

Ile Glu Gly Arg His Met Ala Ser Met Ala Leu Leu Lys Asp Ile Ile  
20 25 30

Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln  
35 40 45

Asn Arg Lys Asn Thr Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val  
50 55 60

Ser Glu Glu Gly Asp Val Gln Leu Asn Pro Ile Phe Pro Phe Asp Phe  
65 70 75 80

Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly Lys Val Ile Val Thr Gln  
85 90 95

Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr Glu Ser Phe Ser Ile Ser  
100 105 110

Phe Trp Ile Arg Ile Asn Lys Trp Val Ser Asn Leu Pro Gly Tyr Thr  
115 120 125

Ile Ile Asp Ser Val Lys Asn Asn Ser Gly Trp Ser Ile Gly Ile Ile  
130 135 140

Ser Asn Phe Leu Val Phe Thr Leu Lys Gln Asn Glu Asp Ser Glu Gln  
145 150 155 160

Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn Asn Ala Pro Gly Tyr Asn  
165 170 175

Lys Trp Phe Phe Val Thr Val Thr Asn Asn Met Met Gly Asn Met Lys  
180 185 190

Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr Ile Lys Val Lys Glu Leu  
195 200 205

Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr Phe Glu Ile Asn Lys Ile  
210 215 220

Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser Asp Asn Ile Asn Met Trp  
225 230 235 240

Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu Leu Asp Gly Lys Asp Ile  
245 250 255

Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr Asn Val Val Lys Asp Tyr  
 260 265 270  
 Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr Met Val Asn Ile  
 275 280 285  
 Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn Ser Arg Gln Ile Val Phe  
 290 295 300  
 Asn Thr Arg Arg Asn Asn Asp Phe Asn Glu Gly Tyr Lys Ile Ile  
 305 310 315 320  
 Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp Thr Arg Val Arg Gly Gly  
 325 330 335  
 Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn Asn Lys Ala Tyr Asn Leu  
 340 345 350  
 Phe Met Lys Asn Glu Thr Met Tyr Ala Asp Asn His Ser Thr Glu Asp  
 355 360 365  
 Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr Lys Asp Ile Asn Asp Asn  
 370 375 380  
 Ile Ile Phe Gln Ile Gln Pro Met Asn Asn Thr Tyr Tyr Tyr Ala Ser  
 385 390 395 400  
 Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu Asn Ile Ser Gly Ile Cys  
 405 410 415  
 Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly Gly Asp Trp Tyr Arg His  
 420 425 430  
 Asn Tyr Leu Val Pro Thr Val Lys Gln Gly Asn Tyr Ala Ser Leu Leu  
 435 440 445  
 Glu Ser Thr Ser Thr His Trp Gly Phe Val Pro Val Ser Glu  
 450 455 460

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CGCCATGGCT TTATTAAAAG ATATAATTAA TG

32

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCAAGCTTTT ATTCACTTAC AGGTACAAAA CC

32

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3831 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..3828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATG ACA TGG CCA GTA AAA GAT TTT AAT TAT AGT GAT CCT GTT AAT GAC Met Thr Trp Pro Val Lys Asp Phe Asn Tyr Ser Asp Pro Val Asn Asp 1 5 10 15	48
AAT GAT ATA TTA TAT TTA AGA ATA CCA CAA AAT AAG TTA ATT ACT ACA Asn Asp Ile Leu Tyr Leu Arg Ile Pro Gln Asn Lys Leu Ile Thr Thr 20 25 30	96
CCT GTA AAA GCT TTT ATG ATT ACT CAA AAT ATT TGG GTA ATA CCA GAA Pro Val Lys Ala Phe Met Ile Thr Gln Asn Ile Trp Val Ile Pro Glu 35 40 45	144
AGA TTT TCA TCA GAT ACT AAT CCA AGT TTA AGT AAA CCG CCC AGA CCT Arg Phe Ser Ser Asp Thr Asn Pro Ser Leu Ser Lys Pro Pro Arg Pro 50 55 60	192
ACT TCA AAG TAT CAA AGT TAT TAT GAT CCT AGT TAT TTA TCT ACT GAT Thr Ser Lys Tyr Gln Ser Tyr Tyr Asp Pro Ser Tyr Leu Ser Thr Asp 65 70 75 80	240
GAA CAA AAA GAT ACA TTT TTA AAA GGG ATT ATA AAA TTA TTT AAA AGA Glu Gln Lys Asp Thr Phe Leu Lys Gly Ile Ile Lys Leu Phe Lys Arg 85 90 95	288
ATT AAT GAA AGA GAT ATA GGA AAA AAA TTA ATA AAT TAT TTA GTA GTT Ile Asn Glu Arg Asp Ile Gly Lys Lys Leu Ile Asn Tyr Leu Val Val 100 105 110	336

GGT TCA CCT TTT ATG GGA GAT TCA AGT ACG CCT GAA GAT ACA TTT GAT Gly Ser Pro Phe Met Gly Asp Ser Ser Thr Pro Glu Asp Thr Phe Asp 115 120 125	384
TTT ACA CGT CAT ACT ACT AAT ATT GCA GTT GAA AAG TTT GAA AAT GGT Phe Thr Arg His Thr Thr Asn Ile Ala Val Glu Lys Phe Glu Asn Gly 130 135 140	432
AGT TGG AAA GTA ACA AAT ATT ATA ACA CCA AGT GTA TTG ATA TTT GGA Ser Trp Lys Val Thr Asn Ile Ile Thr Pro Ser Val Leu Ile Phe Gly 145 150 155 160	480
CCA CTT CCT AAT ATA TTA GAC TAT ACA GCA TCC CTT ACA TTG CAA GGA Pro Leu Pro Asn Ile Leu Asp Tyr Thr Ala Ser Leu Thr Leu Gln Gly 165 170 175	528
CAA CAA TCA AAT CCA TCA TTT GAA GGG TTT GGA ACA TTA TCT ATA CTA Gln Gln Ser Asn Pro Ser Phe Glu Gly Phe Gly Thr Leu Ser Ile Leu 180 185 190	576
AAA GTA GCA CCT GAA TTT TTG TTA ACA TTT AGT GAT GTA ACA TCT AAT Lys Val Ala Pro Glu Phe Leu Leu Thr Phe Ser Asp Val Thr Ser Asn 195 200 205	624
CAA AGT TCA GCT GTA TTA GGC AAA TCT ATA TTT TGT ATG GAT CCA GTA Gln Ser Ser Ala Val Leu Gly Lys Ser Ile Phe Cys Met Asp Pro Val 210 215 220	672
ATA GCT TTA ATG CAT GAG TTA ACA CAT TCT TTG CAT CAA TTA TAT GGA Ile Ala Leu Met His Glu Leu Thr His Ser Leu His Gln Leu Tyr Gly 225 230 235 240	720
ATA AAT ATA CCA TCT GAT AAA AGG ATT CGT CCA CAA GTT AGC GAG GGA Ile Asn Ile Pro Ser Asp Lys Arg Ile Arg Pro Gln Val Ser Glu Gly 245 250 255	768
TTT TTC TCT CAA GAT GGA CCC AAC GTA CAA TTT GAG GAA TTA TAT ACA Phe Phe Ser Gln Asp Gly Pro Asn Val Gln Phe Glu Glu Leu Tyr Thr 260 265 270	816
TTT GGA GGA TTA GAT GTT GAA ATA ATA CCT CAA ATT GAA AGA TCA CAA Phe Gly Gly Leu Asp Val Glu Ile Ile Pro Gln Ile Glu Arg Ser Gln 275 280 285	864
TTA AGA GAA AAA GCA TTA GGT CAC TAT AAA GAT ATA GCG AAA AGA CTT Leu Arg Glu Lys Ala Leu Gly His Tyr Lys Asp Ile Ala Lys Arg Leu 290 295 300	912
AAT AAT ATT AAT AAA ACT ATT CCT TCT AGT TGG ATT AGT AAT ATA GAT Asn Asn Ile Asn Lys Thr Ile Pro Ser Ser Trp Ile Ser Asn Ile Asp 305 310 315 320	960
AAA TAT AAA AAA ATA TTT TCT GAA AAG TAT AAT TTT GAT AAA GAT AAT Lys Tyr Lys Lys Ile Phe Ser Glu Lys Tyr Asn Phe Asp Lys Asp Asn 325 330 335	1008
ACA GGA AAT TTT GTT GTA AAT ATT GAT AAA TTC AAT AGC TTA TAT TCA Thr Gly Asn Phe Val Val Asn Ile Asp Lys Phe Asn Ser Leu Tyr Ser 340 345 350	1056

GAC TTG ACT AAT GTT ATG TCA GAA GTT TAT TCT TCG CAA TAT AAT Asp Leu Thr Asn Val Met Ser Glu Val Val Tyr Ser Ser Gln Tyr Asn 355 360 365	1104
GTT AAA AAC AGG ACT CAT TAT TTT TCA AGG CAT TAT CTA CCT GTA TTT Val Lys Asn Arg Thr His Tyr Phe Ser Arg His Tyr Leu Pro Val Phe 370 375 380	1152
GCA AAT ATA TTA GAT GAT AAT ATT TAT ACT ATA AGA GAT GGT TTT AAT Ala Asn Ile Leu Asp Asp Asn Ile Tyr Thr Ile Arg Asp Gly Phe Asn 385 390 395 400	1200
TTA ACA AAT AAA GGT TTT AAT ATA GAA AAT TCG GGT CAG AAT ATA GAA Leu Thr Asn Lys Gly Phe Asn Ile Glu Asn Ser Gly Gln Asn Ile Glu 405 410 415	1248
AGG AAT CCT GCA CTA CAA AAG CTT AGT TCA GAA AGT GTA GTA GAT TTA Arg Asn Pro Ala Leu Gln Lys Leu Ser Ser Glu Ser Val Val Asp Leu 420 425 430	1296
TTT ACA AAA GTA TGT TTA AGA TTA ACA AAA AAT AGT AGA GAT GAT TCA Phe Thr Lys Val Cys Leu Arg Leu Thr Lys Asn Ser Arg Asp Asp Ser 435 440 445	1344
ACA TGT ATT AAA GTT AAA AAT AAT AGA TTA CCT TAT GTA GCT GAT AAA Thr Cys Ile Lys Val Lys Asn Asn Arg Leu Pro Tyr Val Ala Asp Lys 450 455 460	1392
GAT AGC ATT TCA CAA GAA ATA TTT GAA AAT AAA ATT ATT ACA GAT GAG Asp Ser Ile Ser Gln Glu Ile Phe Glu Asn Lys Ile Ile Thr Asp Glu 465 470 475 480	1440
ACT AAT GTA CAA AAT TAT TCA GAT AAT TTT TCA TTA GAT GAA TCT ATT Thr Asn Val Gln Asn Tyr Ser Asp Asn Phe Ser Leu Asp Glu Ser Ile 485 490 495	1488
TTA GAT GGG CAA GTT CCT ATT AAT CCT GAA ATA GTA GAT CCA CTA TTA Leu Asp Gly Gln Val Pro Ile Asn Pro Glu Ile Val Asp Pro Leu Leu 500 505 510	1536
CCC AAT GTT AAT ATG GAA CCT TTA AAT CTT CCA GGT GAA GAA ATA GTA Pro Asn Val Asn Met Glu Pro Leu Asn Leu Pro Gly Glu Glu Ile Val 515 520 525	1584
TTT TAT GAT GAT ATT ACT AAA TAT GTT GAT TAT TTA AAT TCT TAT TAT Phe Tyr Asp Asp Ile Thr Lys Tyr Val Asp Tyr Leu Asn Ser Tyr Tyr 530 535 540	1632
TAT TTG GAA TCT CAA AAA TTA AGT AAT AAT GTT GAA AAT ATT ACT CTT Tyr Leu Glu Ser Gln Lys Leu Ser Asn Asn Val Glu Asn Ile Thr Leu 545 550 555 560	1680
ACA ACT TCA GTT GAA GAA GCA TTA GGT TAT AGC AAT AAG ATA TAC ACA Thr Thr Ser Val Glu Glu Ala Leu Gly Tyr Ser Asn Lys Ile Tyr Thr 565 570 575	1728
TTT TTA CCT AGC TTA GCT GAA AAA GTG AAT AAA GGT GTT CAA GCA GGT Phe Leu Pro Ser Leu Ala Glu Lys Val Asn Lys Gly Val Gln Ala Gly 580 585 590	1776

TTA TTC TTA AAT TGG GCG AAT GAA GTA GTT GAG GAT TTT ACT ACA AAT Leu Phe Leu Asn Trp Ala Asn Glu Val Val Glu Asp Phe Thr Thr Asn 595 600 605	1824
ATT ATG AAG AAA GAT ACA TTG GAT AAA ATA TCA GAT GTA TCA GTA ATA Ile Met Lys Lys Asp Thr Leu Asp Lys Ile Ser Asp Val Ser Val Ile 610 615 620	1872
ATT CCA TAT ATA GGA CCT GCC TTA AAT ATA GGA AAT TCA GCA TTA AGG Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn Ser Ala Leu Arg 625 630 635 640	1920
GGA AAT TTT AAG CAA GCA TTT GCA ACA GCT GGT GTA GCT TTT TTA TTA Gly Asn Phe Lys Gln Ala Phe Ala Thr Ala Gly Val Ala Phe Leu Leu 645 650 655	1968
GAG GGA TTT CCA GAG TTT ACT ATA CCT GCA CTC GGT GTA TTT ACC TTT Glu Gly Phe Pro Glu Phe Thr Ile Pro Ala Leu Gly Val Phe Thr Phe 660 665 670	2016
TAT AGT TCT ATT CAA GAA AGA GAG AAA ATT ATT AAA ACT ATA GAA AAT Tyr Ser Ser Ile Gln Glu Arg Glu Lys Ile Ile Lys Thr Ile Glu Asn 675 680 685	2064
TGT TTG GAA CAA AGA GTT AAG AGA TGG AAA GAT TCA TAT CAA TGG ATG Cys Leu Glu Gln Arg Val Lys Arg Trp Lys Asp Ser Tyr Gln Trp Met 690 695 700	2112
GTA TCA AAT TGG TTG TCA AGA ATT ACT ACT CAA TTT AAT CAT ATA AAT Val Ser Asn Trp Leu Ser Arg Ile Thr Thr Gln Phe Asn His Ile Asn 705 710 715 720	2160
TAT CAA ATG TAT GAT TCT TTA AGT TAT CAG GCA GAT GCA ATC AAA GCT Tyr Gln Met Tyr Asp Ser Leu Ser Tyr Gln Ala Asp Ala Ile Lys Ala 725 730 735	2208
AAA ATA GAT TTA GAA TAT AAA AAA TAC TCA GGA AGT GAT AAA GAA AAT Lys Ile Asp Leu Glu Tyr Lys Lys Tyr Ser Gly Ser Asp Lys Glu Asn 740 745 750	2256
ATA AAA AGT CAA GTT GAA AAT TTA AAA AAT AGT TTA GAT GTA AAA ATT Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu Asp Val Lys Ile 755 760 765	2304
TCG GAA GCA ATG AAT AAT ATA AAT AAA TTT ATA CGA GAA TGT TCT GTA Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg Glu Cys Ser Val 770 775 780	2352
ACA TAC TTA TTT AAA AAT ATG CTC CCT AAA GTA ATT GAC GAA TTA AAT Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile Asp Glu Leu Asn 785 790 795 800	2400
AAG TTT GAT TTA AGA ACT AAA ACA GAA TTA ATT AAT CTT ATA GAT AGT Lys Phe Asp Leu Arg Thr Lys Thr Glu Leu Ile Asn Leu Ile Asp Ser 805 810 815	2448
CAT AAT ATT ATT CTA GTT GGT GAA GTA GAT AGA TTA AAA GCA AAA GTA His Asn Ile Ile Leu Val Gly Glu Val Asp Arg Leu Lys Ala Lys Val 820 825 830	2496

AAT GAG AGT TTT GAA AAT ACA ATG CCT TTT AAT ATT TTT TCA TAT ACT Asn Glu Ser Phe Glu Asn Thr Met Pro Phe Asn Ile Phe Ser Tyr Thr 835 840 845	2544
AAT AAT TCT TTA AAA GAT ATA ATT AAT GAA TAT TTC AAT AGT ATT Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe Asn Ser Ile 850 855 860	2592
AAT GAT TCA AAA ATT TTG AGC TTA CAA AAC AAA AAA AAT GCT TTA GTG Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Lys Lys Asn Ala Leu Val 865 870 875 880	2640
GAT ACA TCA GGA TAT AAT GCA GAA GTG AGG GTA GGA GAT AAT GTT CAA Asp Thr Ser Gly Tyr Asn Ala Glu Val Arg Val Gly Asp Asn Val Gln 885 890 895	2688
CTT AAT ACG ATA TAT ACA AAT GAC TTT AAA TTA AGT AGT TCA GGA GAT Leu Asn Thr Ile Tyr Thr Asn Asp Phe Lys Leu Ser Ser Ser Gly Asp 900 905 910	2736
AAA ATT ATA GTA AAT TTA AAT AAT ATT TTA TAT AGC GCT ATT TAT Lys Ile Ile Val Asn Leu Asn Asn Ile Leu Tyr Ser Ala Ile Tyr 915 920 925	2784
GAG AAC TCT AGT GTT AGT TTT TGG ATT AAG ATA TCT AAA GAT TTA ACT Glu Asn Ser Ser Val Ser Phe Trp Ile Lys Ile Ser Lys Asp Leu Thr 930 935 940	2832
AAT TCT CAT AAT GAA TAT ACA ATA ATT AAC AGT ATA GAA CAA AAT TCT Asn Ser His Asn Glu Tyr Thr Ile Ile Asn Ser Ile Glu Gln Asn Ser 945 950 955 960	2880
GGG TGG AAA TTA TGT ATT AGG AAT GGC AAT ATA GAA TGG ATT TTA CAA Gly Trp Lys Leu Cys Ile Arg Asn Gly Asn Ile Glu Trp Ile Leu Gln 965 970 975	2928
GAT GTT AAT AGA AAG TAT AAA AGT TTA ATT TTT GAT TAT AGT GAA TCA Asp Val Asn Arg Lys Tyr Lys Ser Leu Ile Phe Asp Tyr Ser Glu Ser 980 985 990	2976
TTA AGT CAT ACA GGA TAT ACA AAT AAA TGG TTT TTT GTT ACT ATA ACT Leu Ser His Thr Gly Tyr Thr Asn Lys Trp Phe Phe Val Thr Ile Thr 995 1000 1005	3024
AAT AAT ATA ATG GGG TAT ATG AAA CTT TAT ATA AAT GGA GAA TTA AAG Asn Asn Ile Met Gly Tyr Met Lys Leu Tyr Ile Asn Gly Glu Leu Lys 1010 1015 1020	3072
CAG AGT CAA AAA ATT GAA GAT TTA GAT GAG GTT AAG TTA GAT AAA ACC Gln Ser Gln Lys Ile Glu Asp Leu Asp Glu Val Lys Leu Asp Lys Thr 1025 1030 1035 1040	3120
ATA GTA TTT GGA ATA GAT GAG AAT ATA GAT GAG AAT CAG ATG CTT TGG Ile Val Phe Gly Ile Asp Glu Asn Ile Asp Glu Asn Gln Met Leu Trp 1045 1050 1055	3168
ATT AGA GAT TTT AAT ATT TTT TCT AAA GAA TTA AGT AAT GAA GAT ATT Ile Arg Asp Phe Asn Ile Phe Ser Lys Glu Leu Ser Asn Glu Asp Ile 1060 1065 1070	3216

AAT ATT GTA TAT GAG GGA CAA ATA TTA AGA AAT GTT ATT AAA GAT TAT Asn Ile Val Tyr Glu Gly Gln Ile Leu Arg Asn Val Ile Lys Asp Tyr 1075 1080 1085	3264
TGG GGA AAT CCT TTG AAG TTT GAT ACA GAA TAT TAT ATT ATT AAT GAT Trp Gly Asn Pro Leu Lys Phe Asp Thr Glu Tyr Tyr Ile Ile Asn Asp 1090 1095 1100	3312
AAT TAT ATA GAT AGG TAT ATT GCA CCT GAA AGT AAT GTA CTT GTA CTT Asn Tyr Ile Asp Arg Tyr Ile Ala Pro Glu Ser Asn Val Leu Val Leu 1105 1110 1115 1120	3360
GTT CGG TAT CCA GAT AGA TCT AAA TTA TAT ACT GGA AAT CCT ATT ACT Val Arg Tyr Pro Asp Arg Ser Lys Leu Tyr Thr Gly Asn Pro Ile Thr 1125 1130 1135	3408
ATT AAA TCA GTA TCT GAT AAG AAT CCT TAT AGT AGA ATT TTA AAT GGA Ile Lys Ser Val Ser Asp Lys Asn Pro Tyr Ser Arg Ile Leu Asn Gly 1140 1145 1150	3456
GAT AAT ATA ATT CTT CAT ATG TTA TAT AAT AGT AGG AAA TAT ATG ATA Asp Asn Ile Ile Leu His Met Leu Tyr Asn Ser Arg Lys Tyr Met Ile 1155 1160 1165	3504
ATA AGA GAT ACT GAT ACA ATA TAT GCA ACA CAA GGA GGA GAG TGT TCA Ile Arg Asp Thr Asp Thr Ile Tyr Ala Thr Gln Gly Gly Glu Cys Ser 1170 1175 1180	3552
CAA AAT TGT GTA TAT GCA TTA AAA TTA CAG AGT AAT TTA GGT AAT TAT Gln Asn Cys Val Tyr Ala Leu Lys Leu Gln Ser Asn Leu Gly Asn Tyr 1185 1190 1195 1200	3600
GGT ATA GGT ATA TTT AGT ATA AAA AAT ATT GTA TCT AAA AAT AAA TAT Gly Ile Gly Ile Phe Ser Ile Lys Asn Ile Val Ser Lys Asn Lys Tyr 1205 1210 1215	3648
TGT AGT CAA ATT TTC TCT AGT TTT AGG GAA AAT ACA ATG CTT CTA GCA Cys Ser Gln Ile Phe Ser Ser Phe Arg Glu Asn Thr Met Leu Leu Ala 1220 1225 1230	3696
GAT ATA TAT AAA CCT TGG AGA TTT TCT TTT AAA AAT GCA TAC ACG CCA Asp Ile Tyr Lys Pro Trp Arg Phe Ser Phe Lys Asn Ala Tyr Thr Pro 1235 1240 1245	3744
GTT GCA GTA ACT AAT TAT GAA ACA AAA CTA TTA TCA ACT TCA TCT TTT Val Ala Val Thr Asn Tyr Glu Thr Lys Leu Leu Ser Thr Ser Ser Phe 1250 1255 1260	3792
TGG AAA TTT ATT TCT AGG GAT CCA GGA TGG GTA GAG TAA Trp Lys Phe Ile Ser Arg Asp Pro Gly Trp Val Glu 1265 1270 1275	3831

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1276 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Thr Trp Pro Val Lys Asp Phe Asn Tyr Ser Asp Pro Val Asn Asp  
1 5 10 15

Asn Asp Ile Leu Tyr Leu Arg Ile Pro Gln Asn Lys Leu Ile Thr Thr  
20 25 30

Pro Val Lys Ala Phe Met Ile Thr Gln Asn Ile Trp Val Ile Pro Glu  
35 40 45

Arg Phe Ser Ser Asp Thr Asn Pro Ser Leu Ser Lys Pro Pro Arg Pro  
50 55 60

Thr Ser Lys Tyr Gln Ser Tyr Tyr Asp Pro Ser Tyr Leu Ser Thr Asp  
65 70 75 80

Glu Gln Lys Asp Thr Phe Leu Lys Gly Ile Ile Lys Leu Phe Lys Arg  
85 90 95

Ile Asn Glu Arg Asp Ile Gly Lys Leu Ile Asn Tyr Leu Val Val  
100 105 110

Gly Ser Pro Phe Met Gly Asp Ser Ser Thr Pro Glu Asp Thr Phe Asp  
115 120 125

Phe Thr Arg His Thr Thr Asn Ile Ala Val Glu Lys Phe Glu Asn Gly  
130 135 140

Ser Trp Lys Val Thr Asn Ile Ile Thr Pro Ser Val Leu Ile Phe Gly  
145 150 155 160

Pro Leu Pro Asn Ile Leu Asp Tyr Thr Ala Ser Leu Thr Leu Gln Gly  
165 170 175

Gln Gln Ser Asn Pro Ser Phe Glu Gly Phe Gly Thr Leu Ser Ile Leu  
180 185 190

Lys Val Ala Pro Glu Phe Leu Leu Thr Phe Ser Asp Val Thr Ser Asn  
195 200 205

Gln Ser Ser Ala Val Leu Gly Lys Ser Ile Phe Cys Met Asp Pro Val  
210 215 220

Ile Ala Leu Met His Glu Leu Thr His Ser Leu His Gln Leu Tyr Gly  
225 230 235 240

Ile Asn Ile Pro Ser Asp Lys Arg Ile Arg Pro Gln Val Ser Glu Gly  
245 250 255

Phe Phe Ser Gln Asp Gly Pro Asn Val Gln Phe Glu Glu Leu Tyr Thr  
260 265 270

Phe Gly Gly Leu Asp Val Glu Ile Ile Pro Gln Ile Glu Arg Ser Gln  
275 280 285

Leu Arg Glu Lys Ala Leu Gly His Tyr Lys Asp Ile Ala Lys Arg Leu  
290 295 300

Asn Asn Ile Asn Lys Thr Ile Pro Ser Ser Trp Ile Ser Asn Ile Asp  
305 310 315 320

Lys Tyr Lys Lys Ile Phe Ser Glu Lys Tyr Asn Phe Asp Lys Asp Asn  
 325 330 335  
 Thr Gly Asn Phe Val Val Asn Ile Asp Lys Phe Asn Ser Leu Tyr Ser  
 340 345 350  
 Asp Leu Thr Asn Val Met Ser Glu Val Val Tyr Ser Ser Gln Tyr Asn  
 355 360 365  
 Val Lys Asn Arg Thr His Tyr Phe Ser Arg His Tyr Leu Pro Val Phe  
 370 375 380  
 Ala Asn Ile Leu Asp Asp Asn Ile Tyr Thr Ile Arg Asp Gly Phe Asn  
 385 390 395 400  
 Leu Thr Asn Lys Gly Phe Asn Ile Glu Asn Ser Gly Gln Asn Ile Glu  
 405 410 415  
 Arg Asn Pro Ala Leu Gln Lys Leu Ser Ser Glu Ser Val Val Asp Leu  
 420 425 430  
 Phe Thr Lys Val Cys Leu Arg Leu Thr Lys Asn Ser Arg Asp Asp Ser  
 435 440 445  
 Thr Cys Ile Lys Val Lys Asn Asn Arg Leu Pro Tyr Val Ala Asp Lys  
 450 455 460  
 Asp Ser Ile Ser Gln Glu Ile Phe Glu Asn Lys Ile Ile Thr Asp Glu  
 465 470 475 480  
 Thr Asn Val Gln Asn Tyr Ser Asp Asn Phe Ser Leu Asp Glu Ser Ile  
 485 490 495  
 Leu Asp Gly Gln Val Pro Ile Asn Pro Glu Ile Val Asp Pro Leu Leu  
 500 505 510  
 Pro Asn Val Asn Met Glu Pro Leu Asn Leu Pro Gly Glu Glu Ile Val  
 515 520 525  
 Phe Tyr Asp Asp Ile Thr Lys Tyr Val Asp Tyr Leu Asn Ser Tyr Tyr  
 530 535 540  
 Tyr Leu Glu Ser Gln Lys Leu Ser Asn Asn Val Glu Asn Ile Thr Leu  
 545 550 555 560  
 Thr Thr Ser Val Glu Glu Ala Leu Gly Tyr Ser Asn Lys Ile Tyr Thr  
 565 570 575  
 Phe Leu Pro Ser Leu Ala Glu Lys Val Asn Lys Gly Val Gln Ala Gly  
 580 585 590  
 Leu Phe Leu Asn Trp Ala Asn Glu Val Val Glu Asp Phe Thr Thr Asn  
 595 600 605  
 Ile Met Lys Lys Asp Thr Leu Asp Lys Ile Ser Asp Val Ser Val Ile  
 610 615 620  
 Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn Ser Ala Leu Arg  
 625 630 635 640  
 Gly Asn Phe Lys Gln Ala Phe Ala Thr Ala Gly Val Ala Phe Leu Leu  
 645 650 655

Glu Gly Phe Pro Glu Phe Thr Ile Pro Ala Leu Gly Val Phe Thr Phe  
 660 665 670  
 Tyr Ser Ser Ile Gln Glu Arg Glu Lys Ile Ile Lys Thr Ile Glu Asn  
 675 680 685  
 Cys Leu Glu Gln Arg Val Lys Arg Trp Lys Asp Ser Tyr Gln Trp Met  
 690 695 700  
 Val Ser Asn Trp Leu Ser Arg Ile Thr Thr Gln Phe Asn His Ile Asn  
 705 710 715 720  
 Tyr Gln Met Tyr Asp Ser Leu Ser Tyr Gln Ala Asp Ala Ile Lys Ala  
 725 730 735  
 Lys Ile Asp Leu Glu Tyr Lys Tyr Ser Gly Ser Asp Lys Glu Asn  
 740 745 750  
 Ile Lys Ser Gln Val Glu Asn Leu Lys Asn Ser Leu Asp Val Lys Ile  
 755 760 765  
 Ser Glu Ala Met Asn Asn Ile Asn Lys Phe Ile Arg Glu Cys Ser Val  
 770 775 780  
 Thr Tyr Leu Phe Lys Asn Met Leu Pro Lys Val Ile Asp Glu Leu Asn  
 785 790 795 800  
 Lys Phe Asp Leu Arg Thr Lys Thr Glu Leu Ile Asn Leu Ile Asp Ser  
 805 810 815  
 His Asn Ile Ile Leu Val Gly Glu Val Asp Arg Leu Lys Ala Lys Val  
 820 825 830  
 Asn Glu Ser Phe Glu Asn Thr Met Pro Phe Asn Ile Phe Ser Tyr Thr  
 835 840 845  
 Asn Asn Ser Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe Asn Ser Ile  
 850 855 860  
 Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Lys Lys Asn Ala Leu Val  
 865 870 875 880  
 Asp Thr Ser Gly Tyr Asn Ala Glu Val Arg Val Gly Asp Asn Val Gln  
 885 890 895  
 Leu Asn Thr Ile Tyr Thr Asn Asp Phe Lys Leu Ser Ser Gly Asp  
 900 905 910  
 Lys Ile Ile Val Asn Leu Asn Asn Ile Leu Tyr Ser Ala Ile Tyr  
 915 920 925  
 Glu Asn Ser Ser Val Ser Phe Trp Ile Lys Ile Ser Lys Asp Leu Thr  
 930 935 940  
 Asn Ser His Asn Glu Tyr Thr Ile Ile Asn Ser Ile Glu Gln Asn Ser  
 945 950 955 960  
 Gly Trp Lys Leu Cys Ile Arg Asn Gly Asn Ile Glu Trp Ile Leu Gln  
 965 970 975  
 Asp Val Asn Arg Lys Tyr Lys Ser Leu Ile Phe Asp Tyr Ser Glu Ser  
 980 985 990

Leu Ser His Thr Gly Tyr Thr Asn Lys Trp Phe Phe Val Thr Ile Thr  
 995 1000 1005  
 Asn Asn Ile Met Gly Tyr Met Lys Leu Tyr Ile Asn Gly Glu Leu Lys  
 1010 1015 1020  
 Gln Ser Gln Lys Ile Glu Asp Leu Asp Glu Val Lys Leu Asp Lys Thr  
 1025 1030 1035 1040  
 Ile Val Phe Gly Ile Asp Glu Asn Ile Asp Glu Asn Gln Met Leu Trp  
 1045 1050 1055  
 Ile Arg Asp Phe Asn Ile Phe Ser Lys Glu Leu Ser Asn Glu Asp Ile  
 1060 1065 1070  
 Asn Ile Val Tyr Glu Gly Gln Ile Leu Arg Asn Val Ile Lys Asp Tyr  
 1075 1080 1085  
 Trp Gly Asn Pro Leu Lys Phe Asp Thr Glu Tyr Tyr Ile Ile Asn Asp  
 1090 1095 1100  
 Asn Tyr Ile Asp Arg Tyr Ile Ala Pro Glu Ser Asn Val Leu Val Leu  
 1105 1110 1115 1120  
 Val Arg Tyr Pro Asp Arg Ser Lys Leu Tyr Thr Gly Asn Pro Ile Thr  
 1125 1130 1135  
 Ile Lys Ser Val Ser Asp Lys Asn Pro Tyr Ser Arg Ile Leu Asn Gly  
 1140 1145 1150  
 Asp Asn Ile Ile Leu His Met Leu Tyr Asn Ser Arg Lys Tyr Met Ile  
 1155 1160 1165  
 Ile Arg Asp Thr Asp Thr Ile Tyr Ala Thr Gln Gly Gly Glu Cys Ser  
 1170 1175 1180  
 Gln Asn Cys Val Tyr Ala Leu Lys Leu Gln Ser Asn Leu Gly Asn Tyr  
 1185 1190 1195 1200  
 Gly Ile Gly Ile Phe Ser Ile Lys Asn Ile Val Ser Lys Asn Lys Tyr  
 1205 1210 1215  
 Cys Ser Gln Ile Phe Ser Ser Phe Arg Glu Asn Thr Met Leu Leu Ala  
 1220 1225 1230  
 Asp Ile Tyr Lys Pro Trp Arg Phe Ser Phe Lys Asn Ala Tyr Thr Pro  
 1235 1240 1245  
 Val Ala Val Thr Asn Tyr Glu Thr Lys Leu Leu Ser Thr Ser Ser Phe  
 1250 1255 1260  
 Trp Lys Phe Ile Ser Arg Asp Pro Gly Trp Val Glu  
 1265 1270 1275

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 108..1460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

AGATCTCGAT CCCGCGAAAT TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA	60
TTCCCCCTCTA GAAATAATTT TGTTTAACCTT TAAGAAGGG ATATACC ATG GGC CAT Met Gly His 1	116
CAT CAT CAT CAT CAT CAT CAC AGC AGC GGC CAT ATC GAA GGT His His His His His His Ser Ser Gly His Ile Glu Gly 5 10 15	164
CGT CAT ATG GCT AGC ATG GCT TTA TTA AAA GAT ATA ATT AAT GAA TAT Arg His Met Ala Ser Met Ala Leu Leu Lys Asp Ile Ile Asn Glu Tyr 20 25 30 35	212
TTC AAT AGT ATT AAT GAT TCA AAA ATT TTG AGC TTA CAA AAC AAA AAA Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln Asn Lys Lys 40 45 50	260
AAT GCT TTA GTG GAT ACA TCA GGA TAT AAT GCA GAA GTG AGG GTA GGA Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val Arg Val Gly 55 60 65	308
GAT AAT GTT CAA CTT AAT ACG ATA TAT ACA AAT GAC TTT AAA TTA AGT Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn Asp Phe Lys Leu Ser 70 75 80	356
AGT TCA GGA GAT AAA ATT ATA GTA AAT TTA AAT AAT AAT ATT TTA TAT Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn Asn Ile Leu Tyr 85 90 95	404
AGC GCT ATT TAT GAG AAC TCT AGT GTT AGT TTT TGG ATT AAG ATA TCT Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe Trp Ile Lys Ile Ser 100 105 110 115	452
AAA GAT TTA ACT AAT TCT CAT AAT GAA TAT ACA ATA ATT AAC AGT ATA Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr Ile Ile Asn Ser Ile 120 125 130	500
GAA CAA AAT TCT GGG TGG AAA TTA TGT ATT AGG AAT GGC AAT ATA GAA Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg Asn Gly Asn Ile Glu 135 140 145	548
TGG ATT TTA CAA GAT GTT AAT AGA AAG TAT AAA AGT TTA ATT TTT GAT Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys Ser Leu Ile Phe Asp 150 155 160	596

TAT AGT GAA TCA TTA AGT CAT ACA GGA TAT ACA AAT AAA TGG TTT TTT Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr Asn Lys Trp Phe Phe 165 170 175	644
GTT ACT ATA ACT AAT AAT ATA ATG GGG TAT ATG AAA CTT TAT ATA AAT Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met Lys Leu Tyr Ile Asn 180 185 190 195	692
GGA GAA TTA AAG CAG AGT CAA AAA ATT GAA GAT TTA GAT GAG GTT AAG Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp Leu Asp Glu Val Lys 200 205 210	740
TTA GAT AAA ACC ATA GTA TTT GGA ATA GAT GAG AAT ATA GAT GAG AAT Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu Asn Ile Asp Glu Asn 215 220 225	788
CAG ATG CTT TGG ATT AGA GAT TTT AAT ATT TTT TCT AAA GAA TTA AGT Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe Ser Lys Glu Leu Ser 230 235 240	836
AAT GAA GAT ATT AAT ATT GTA TAT GAG GGA CAA ATA TTA AGA AAT GTT Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln Ile Leu Arg Asn Val 245 250 255	884
ATT AAA GAT TAT TGG GGA AAT CCT TTG AAG TTT GAT ACA GAA TAT TAT Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe Asp Thr Glu Tyr Tyr 260 265 270 275	932
ATT ATT AAT GAT AAT TAT ATA GAT AGG TAT ATT GCA CCT GAA AGT AAT Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile Ala Pro Glu Ser Asn 280 285 290	980
GTA CTT GTA CTT GTT CGG TAT CCA GAT AGA TCT AAA TTA TAT ACT GGA Val Leu Val Leu Val Arg Tyr Pro Asp Arg Ser Lys Leu Tyr Thr Gly 295 300 305	1028
AAT CCT ATT ACT ATT AAA TCA GTA TCT GAT AAG AAT CCT TAT AGT AGA Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys Asn Pro Tyr Ser Arg 310 315 320	1076
ATT TTA AAT GGA GAT AAT ATA ATT CTT CAT ATG TTA TAT AAT AGT AGG Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met Leu Tyr Asn Ser Arg 325 330 335	1124
AAA TAT ATG ATA ATA AGA GAT ACT GAT ACA ATA TAT GCA ACA CAA GGA Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile Tyr Ala Thr Gln Gly 340 345 350 355	1172
GGA GAG TGT TCA CAA AAT TGT GTA TAT GCA TTA AAA TTA CAG AGT AAT Gly Glu Cys Ser Gln Asn Cys Val Tyr Ala Leu Lys Leu Gln Ser Asn 360 365 370	1220
TTA GGT AAT TAT GGT ATA GGT ATA TTT AGT ATA AAA AAT ATT GTA TCT Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile Lys Asn Ile Val Ser 375 380 385	1268
AAA AAT AAA TAT TGT AGT CAA ATT TTC TCT AGT TTT AGG GAA AAT ACA Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser Phe Arg Glu Asn Thr 390 395 400	1316

ATG CTT CTA GCA GAT ATA TAT AAA CCT TGG AGA TTT TCT TTT AAA AAT	1364		
Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg Phe Ser Phe Lys Asn			
405	410	415	
GCA TAC ACG CCA GTT GCA GTA ACT AAT TAT GAA ACA AAA CTA TTA TCA	1412		
Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu Thr Lys Leu Leu Ser			
420	425	430	435
ACT TCA TCT TTT TGG AAA TTT ATT TCT AGG GAT CCA GGA TGG GTA GAG	1460		
Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp Pro Gly Trp Val Glu			
440	445	450	
<b>TAAAAAGCTT</b>	1469		

(2) INFOR

1469

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Gly His His His His His His His His Ser Ser Gly His  
1 5 10 15

Ile Glu Gly Arg His Met Ala Ser Met Ala Leu Leu Lys Asp Ile Ile  
20 25 30

Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln  
35 40 45

Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val  
50 . . . . . 55 . . . . . 60 . . . . .

Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn Asp Phe  
65                   70                   75                   80

Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn Asn Asn  
85 90 95

Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe Trp Ile  
100 105 110

Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr Ile Ile  
115 120 125

Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg Asn Gly  
130 135 140

Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys Ser Leu  
145 150 155 160

Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr Asn Lys  
165 170 175

Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met Lys Leu  
189 190 191 192 193 194 195 196 197 198 199 200 201 202

Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp Leu Asp  
 195 200 205  
 Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu Asn Ile  
 210 215 220  
 Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe Ser Lys  
 225 230 235 240  
 Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln Ile Leu  
 245 250 255  
 Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe Asp Thr  
 260 265 270  
 Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile Ala Pro  
 275 280 285  
 Glu Ser Asn Val Leu Val Leu Val Arg Tyr Pro Asp Arg Ser Lys Leu  
 290 295 300  
 Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys Asn Pro  
 305 310 315 320  
 Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met Leu Tyr  
 325 330 335  
 Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile Tyr Ala  
 340 345 350  
 Thr Gln Gly Gly Glu Cys Ser Gln Asn Cys Val Tyr Ala Leu Lys Leu  
 355 360 365  
 Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile Lys Asn  
 370 375 380  
 Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser Phe Arg  
 385 390 395 400  
 Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg Phe Ser  
 405 410 415  
 Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu Thr Lys  
 420 425 430  
 Leu Leu Ser Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp Pro Gly  
 435 440 445  
 Trp Val Glu  
 450

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GCAAGCTTTT ACTCTACCCA TCCTGGATCC CT

32

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3825 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATG CCA GTT GCA ATA AAT AGT TTT AAT TAT AAT GAC CCT GTT AAT GAT Met Pro Val Ala Ile Asn Ser Phe Asn Tyr Asn Asp Pro Val Asn Asp	48
1 5 10 15	
GAT ACA ATT TTA TAC ATG CAG ATA CCA TAT GAA GAA AAA AGT AAA AAA Asp Thr Ile Leu Tyr Met Gln Ile Pro Tyr Glu Glu Lys Ser Lys Lys	96
20 25 30	
TAT TAT AAA GCT TTT GAG ATT ATG CGT AAT GTT TGG ATA ATT CCT GAG Tyr Tyr Lys Ala Phe Glu Ile Met Arg Asn Val Trp Ile Ile Pro Glu	144
35 40 45	
AGA AAT ACA ATA GGA ACG AAT CCT AGT GAT TTT GAT CCA CCG GCT TCA Arg Asn Thr Ile Gly Thr Asn Pro Ser Asp Phe Asp Pro Pro Ala Ser	192
50 55 60	
TTA AAG AAC GGA AGC AGT GCT TAT TAT GAT CCT AAT TAT TTA ACC ACT Leu Lys Asn Gly Ser Ser Ala Tyr Tyr Asp Pro Asn Tyr Leu Thr Thr	240
65 70 75 80	
GAT GCT GAA AAA GAT AGA TAT TTA AAA ACA ACG ATA AAA TTA TTT AAG Asp Ala Glu Lys Asp Arg Tyr Leu Lys Thr Thr Ile Lys Leu Phe Lys	288
85 90 95	
AGA ATT AAT AGT AAT CCT GCA GGG AAA GTT TTG TTA CAA GAA ATA TCA Arg Ile Asn Ser Asn Pro Ala Gly Lys Val Leu Leu Gln Glu Ile Ser	336
100 105 110	
TAT GCT AAA CCA TAT TTA GGA AAT GAC CAC ACG CCA ATT GAT GAA TTC Tyr Ala Lys Pro Tyr Leu Gly Asn Asp His Thr Pro Ile Asp Glu Phe	384
115 120 125	
TCT CCA GTT ACT AGA ACT ACA AGT GTT AAT ATA AAA TTA TCA ACT AAT Ser Pro Val Thr Arg Thr Ser Val Asn Ile Lys Leu Ser Thr Asn	432
130 135 140	
GTT GAA AGT TCA ATG TTA TTG AAT CTT CTT GTA TTG GGA GCA GGA CCT Val Glu Ser Ser Met Leu Leu Asn Leu Leu Leu Gly Ala Gly Pro	480
145 150 155 160	

GAT ATA TTT GAA AGT TGT TGT TAC CCC GTT AGA AAA CTA ATA GAT CCA Asp Ile Phe Glu Ser Cys Cys Tyr Pro Val Arg Lys Leu Ile Asp Pro 165 170 175	528
GAT GTA GTT TAT GAT CCA AGT AAT TAT GGT TTT GGA TCA ATT AAT ATC Asp Val Val Tyr Asp Pro Ser Asn Tyr Gly Phe Gly Ser Ile Asn Ile 180 185 190	576
GTG ACA TTT TCA CCT GAG TAT GAA TAT ACT TTT AAT GAT ATT AGT GGA Val Thr Phe Ser Pro Glu Tyr Glu Tyr Thr Phe Asn Asp Ile Ser Gly 195 200 205	624
GGG CAT AAT AGT AGT ACA GAA TCA TTT ATT GCA GAT CCT GCA ATT TCA Gly His Asn Ser Ser Thr Glu Ser Phe Ile Ala Asp Pro Ala Ile Ser 210 215 220	672
CTA GCT CAT GAA TTG ATA CAT GCA CTG CAT GGA TTA TAC GGG GCT AGG Leu Ala His Glu Leu Ile His Ala Leu His Gly Leu Tyr Gly Ala Arg 225 230 235 240	720
GGA GTT ACT TAT GAA GAG ACT ATA GAA GTA AAG CAA GCA CCT CTT ATG Gly Val Thr Tyr Glu Glu Thr Ile Glu Val Lys Gln Ala Pro Leu Met 245 250 255	768
ATA GCC GAA AAA CCC ATA AGG CTA GAA GAA TTT TTA ACC TTT GGA GGT Ile Ala Glu Lys Pro Ile Arg Leu Glu Glu Phe Leu Thr Phe Gly Gly 260 265 270	816
CAG GAT TTA AAT ATT ATT ACT AGT GCT ATG AAG GAA AAA ATA TAT AAC Gln Asp Leu Asn Ile Ile Thr Ser Ala Met Lys Glu Lys Ile Tyr Asn 275 280 285	864
AAT CTT TTA GCT AAC TAT GAA AAA ATA GCT ACT AGA CTT AGT GAA GTT Asn Leu Leu Ala Asn Tyr Glu Lys Ile Ala Thr Arg Leu Ser Glu Val 290 295 300	912
AAT AGT GCT CCT GAA TAT GAT ATT AAT GAA TAT AAA GAT TAT TTT Asn Ser Ala Pro Pro Glu Tyr Asp Ile Asn Glu Tyr Lys Asp Tyr Phe 305 310 315 320	960
CAA TGG AAG TAT GGG CTA GAT AAA AAT GCT GAT GGA AGT TAT ACT GTA Gln Trp Lys Tyr Gly Leu Asp Lys Asn Ala Asp Gly Ser Tyr Thr Val 325 330 335	1008
AAT GAA AAT AAA TTT AAT GAA ATT TAT AAA AAA TTA TAT AGT TTT ACA Asn Glu Asn Lys Phe Asn Glu Ile Tyr Lys Lys Leu Tyr Ser Phe Thr 340 345 350	1056
GAG AGT GAC TTA GCA AAT AAA TTT AAA GTA AAA TGT AGA AAT ACT TAT Glu Ser Asp Leu Ala Asn Lys Phe Lys Val Lys Cys Arg Asn Thr Tyr 355 360 365	1104
TTT ATT AAA TAT GAA TTT TTA AAA GTT CCA AAT TTG TTA GAT GAT GAT Phe Ile Lys Tyr Glu Phe Leu Lys Val Pro Asn Leu Asp Asp Asp 370 375 380	1152
ATT TAT ACT GTA TCA GAG CGG TTT AAT ATA GGT AAT TTA GCA GTA AAC Ile Tyr Thr Val Ser Glu Gly Phe Asn Ile Gly Asn Leu Ala Val Asn 385 390 395 400	1200

AAT CGC GGA CAA AGT ATA AAG TTA AAT CCT AAA ATT ATT GAT TCC ATT Asn Arg Gly Gln Ser Ile Lys Leu Asn Pro Lys Ile Ile Asp Ser Ile 405 410 415	1248
CCA GAT AAA GGT CTA GTA GAA AAG ATC GTT AAA TTT TGT AAG AGC GTT Pro Asp Lys Gly Leu Val Glu Lys Ile Val Lys Phe Cys Lys Ser Val 420 425 430	1296
ATT CCT AGA AAA GGT ACA AAG GCG CCA CCG CGA CTA TGC ATT AGA GTA Ile Pro Arg Lys Gly Thr Lys Ala Pro Pro Arg Leu Cys Ile Arg Val 435 440 445	1344
AAT AAT AGT GAG TTA TTT GTT GCT TCA GAA AGT AGC TAT AAT GAA Asn Asn Ser Glu Leu Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu 450 455 460	1392
AAT GAT ATT AAT ACA CCT AAA GAA ATT GAC GAT ACA ACA AAT CTA AAT Asn Asp Ile Asn Thr Pro Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn 465 470 475 480	1440
AAT AAT TAT AGA AAT AAT TTA GAT GAA GTT ATT TTA GAT TAT AAT AGT Asn Asn Tyr Arg Asn Asn Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser 485 490 495	1488
CAG ACA ATA CCT CAA ATA TCA AAT CGA ACA TTA AAT ACA CTT GTA CAA Gln Thr Ile Pro Gln Ile Ser Asn Arg Thr Leu Asn Thr Leu Val Gln 500 505 510	1536
GAC AAT AGT TAT GTG CCA AGA TAT GAT TCT AAT GGA ACA AGT GAA ATA Asp Asn Ser Tyr Val Pro Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile 515 520 525	1584
GAG GAA TAT GAT GTT GTT GAC TTT AAT GTA TTT TTC TAT TTA CAT GCA Glu Glu Tyr Asp Val Val Asp Phe Asn Val Phe Phe Tyr Leu His Ala 530 535 540	1632
CAA AAA GTG CCA GAA GGT GAA ACC AAT ATA AGT TTA ACT TCT TCA ATT Gln Lys Val Pro Glu Gly Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile 545 550 555 560	1680
GAT ACA GCA TTA TTA GAA GAA TCC AAA GAT ATA TTT TTT TCT TCA GAG Asp Thr Ala Leu Leu Glu Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu 565 570 575	1728
TTT ATC GAT ACT ATC AAT AAA CCT GTA AAT GCA GCA CTA TTT ATA GAT Phe Ile Asp Thr Ile Asn Lys Pro Val Asn Ala Ala Leu Phe Ile Asp 580 585 590	1776
TGG ATA AGC AAA GTA ATA AGA GAT TTT ACC ACT GAA GCT ACA CAA AAA Trp Ile Ser Lys Val Ile Arg Asp Phe Thr Thr Glu Ala Thr Gln Lys 595 600 605	1824
AGT ACT GTT GAT AAG ATT GCA GAC ATA TCT TTA ATT GTA CCC TAT GTA Ser Thr Val Asp Lys Ile Ala Asp Ile Ser Leu Ile Val Pro Tyr Val 610 615 620	1872
GGT CTT GCT TTG AAT ATA ATT ATT GAG GCA GAA AAA GGA AAT TTT GAG Gly Leu Ala Leu Asn Ile Ile Glu Ala Glu Lys Gly Asn Phe Glu 625 630 635 640	1920

GAG GCA TTT GAA TTA TTA GGA GTG GGT ATT TTA TTA GAA TTT GTG CCA Glu Ala Phe Glu Leu Leu Gly Val Gly Ile Leu Leu Glu Phe Val Pro 645 650 655	1968
GAA CTT ACA ATT CCT GTA ATT TTA GTG TTT ACG ATA AAA TCC TAT ATA Glu Leu Thr Ile Pro Val Ile Leu Val Phe Thr Ile Lys Ser Tyr Ile 660 665 670	2016
GAT TCA TAT GAG AAT AAA AAT AAA GCA ATT AAA GCA ATA AAT AAT TCA Asp Ser Tyr Glu Asn Lys Asn Lys Ala Ile Lys Ala Ile Asn Asn Ser 675 680 685	2064
TTA ATC GAA AGA GAA GCA AAG TGG AAA GAA ATA TAT AGT TGG ATA GTA Leu Ile Glu Arg Glu Ala Lys Trp Lys Glu Ile Tyr Ser Trp Ile Val 690 695 700	2112
TCA AAT TGG CTT ACT AGA ATT AAT ACT CAA TTT AAT AAA AGA AAA GAG Ser Asn Trp Leu Thr Arg Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu 705 710 715 720	2160
CAA ATG TAT CAG GCT TTA CAA AAT CAA GTA GAT GCA ATA AAA ACA GCA Gln Met Tyr Gln Ala Leu Gln Asn Gln Val Asp Ala Ile Lys Thr Ala 725 730 735	2208
ATA GAA TAT AAA TAT AAT AAT TAT ACT TCA GAT GAG AAA AAT AGA CTT Ile Glu Tyr Lys Tyr Asn Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu 740 745 750	2256
GAA TCT GAA TAT AAT ATC AAT AAT ATA GAA GAA GAA TTG AAT AAA AAA Glu Ser Glu Tyr Asn Ile Asn Asn Ile Glu Glu Glu Leu Asn Lys Lys 755 760 765	2304
GTT TCT TTA GCA ATG AAA AAT ATA GAA AGA TTT ATG ACA GAA AGT TCT Val Ser Leu Ala Met Lys Asn Ile Glu Arg Phe Met Thr Glu Ser Ser 770 775 780	2352
ATA TCT TAT TTA ATG AAA TTA ATA AAT GAA GCC AAA GTT GGT AAA TTA Ile Ser Tyr Leu Met Lys Leu Ile Asn Glu Ala Lys Val Gly Lys Leu 785 790 795 800	2400
AAA AAA TAT GAT AAC CAT GTT AAG AGC GAT TTA TTA AAC TAT ATT CTC Lys Lys Tyr Asp Asn His Val Lys Ser Asp Leu Leu Asn Tyr Ile Leu 805 810 815	2448
GAC CAT AGA TCA ATC TTA GGA GAG CAG ACA AAT GAA TTA AGT GAT TTG Asp His Arg Ser Ile Leu Gly Glu Gln Thr Asn Glu Leu Ser Asp Leu 820 825 830	2496
GTG ACT AGT ACT TTG AAT AGT AGT ATT CCA TTT GAA CTT TCT TCA TAT Val Thr Ser Thr Leu Asn Ser Ser Ile Pro Phe Glu Leu Ser Ser Tyr 835 840 845	2544
ACT AAT GAT AAA ATT CTA ATT ATA TAT TTT AAT AGA TTA TAT AAA AAA Thr Asn Asp Lys Ile Leu Ile Ile Tyr Phe Asn Arg Leu Tyr Lys Lys 850 855 860	2592
ATT AAA GAT AGT TCT ATT TTA GAT ATG CGA TAT GAA AAT AAT AAA TTT Ile Lys Asp Ser Ser Ile Leu Asp Met Arg Tyr Glu Asn Asn Lys Phe 865 870 875 880	2640

ATA GAT ATC TCT GGA TAT GGT TCA AAT ATA AGC ATT AAT GGA AAC GTA Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn Gly Asn Val 885 890 895	2688
TAT ATT TAT TCA ACA AAT AGA AAT CAA TTT GGA ATA TAT AAT AGT AGG Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr Asn Ser Arg 900 905 910	2736
CTT AGT GAA GTT AAT ATA GCT CAA AAT AAT GAT ATT ATA TAC AAT AGT Leu Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile Tyr Asn Ser 915 920 925	2784
AGA TAT CAA AAT TTT AGT ATT AGT TTC TGG GTA AGG ATT CCT AAA CAC Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Lys His 930 935 940	2832
TAC AAA CCT ATG AAT CAT AAT CGG GAA TAC ACT ATA ATA AAT TGT ATG Tyr Lys Pro Met Asn His Asn Arg Glu Tyr Thr Ile Ile Asn Cys Met 945 950 955 960	2880
GGG AAT AAT AAT TCG GGA TGG AAA ATA TCA CTT AGA ACT GTT AGA GAT Gly Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Arg Thr Val Arg Asp 965 970 975	2928
TGT GAA ATA ATT TGG ACT TTA CAA GAT ACT TCT GGA AAT AAG GAA AAT Cys Glu Ile Ile Trp Thr Leu Gln Asp Thr Ser Gly Asn Lys Glu Asn 980 985 990	2976
TTA ATT TTT AGG TAT GAA GAA CTT AAT AGG ATA TCT AAT TAT ATA AAT Leu Ile Phe Arg Tyr Glu Glu Leu Asn Arg Ile Ser Asn Tyr Ile Asn 995 1000 1005	3024
AAA TGG ATT TTT GTA ACT ATT ACT AAT AAT AGA TTA GGC AAT TCT AGA Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg 1010 1015 1020	3072
ATT TAC ATC AAT GGA AAT TTA ATA GTT GAA AAA TCA ATT TCG AAT TTA Ile Tyr Ile Asn Gly Asn Leu Ile Val Glu Lys Ser Ile Ser Asn Leu 1025 1030 1035 1040	3120
GGT GAT ATT CAT GTT AGT GAT AAT ATA TTA TTT AAA ATT GTT GGT TGT Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys 1045 1050 1055	3168
GAT GAT GAA ACG TAT GTT GGT ATA AGA TAT TTT AAA GTT TTT AAT ACG Asp Asp Glu Thr Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asn Thr 1060 1065 1070	3216
GAA TTA GAT AAA ACA GAA ATT GAG ACT TTA TAT AGT AAT GAG CCA GAT Glu Leu Asp Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asn Glu Pro Asp 1075 1080 1085	3264
CCA AGT ATC TTA AAA AAC TAT TGG GGA AAT TAT TTG CTA TAT AAT AAA Pro Ser Ile Leu Lys Asn Tyr Trp Gly Asn Tyr Leu Leu Tyr Asn Lys 1090 1095 1100	3312
AAA TAT TAT TTA TTC AAT TTA CTA AGA AAA GAT AAG TAT ATT ACT CTG Lys Tyr Tyr Leu Phe Asn Leu Leu Arg Lys Asp Lys Tyr Ile Thr Leu 1105 1110 1115 1120	3360

AAT TCA GGC ATT TTA AAT ATT AAT CAA CAA AGA GGT GTT ACT GAA GGC Asn Ser Gly Ile Leu Asn Ile Asn Gln Gln Arg Gly Val Thr Glu Gly 1125 1130 1135	3408
TCT GTT TTT TTG AAC TAT AAA TTA TAT GAA GGA GTA GAA GTC ATT ATA Ser Val Phe Leu Asn Tyr Lys Leu Tyr Glu Gly Val Glu Val Ile Ile 1140 1145 1150	3456
AGA AAA AAT GGT CCT ATA GAT ATA TCT AAT ACA GAT AAT TTT GTT AGA Arg Lys Asn Gly Pro Ile Asp Ile Ser Asn Thr Asp Asn Phe Val Arg 1155 1160 1165	3504
AAA AAC GAT CTA GCA TAC ATT AAT GTA GTA GAT CGT GGT GTA GAA TAT Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Gly Val Glu Tyr 1170 1175 1180	3552
CGG TTA TAT GCT GAT ACA AAA TCA GAG AAA GAG AAA ATA ATA AGA ACA Arg Leu Tyr Ala Asp Thr Lys Ser Glu Lys Glu Lys Ile Ile Arg Thr 1185 1190 1195 1200	3600
TCT AAT CTA AAC GAT AGC TTA GGT CAA ATT ATA GTT ATG GAT TCA ATA Ser Asn Leu Asn Asp Ser Leu Gly Gln Ile Ile Val Met Asp Ser Ile 1205 1210 1215	3648
GGA AAT AAT TGC ACA ATG AAT TTT CAA AAC AAT AAT GGG AGC AAT ATA Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn Asn Gly Ser Asn Ile 1220 1225 1230	3696
GGA TTA CTA GGT TTT CAT TCA AAT AAT TTG GTT GCT AGT AGT TGG TAT Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val Ala Ser Ser Trp Tyr 1235 1240 1245	3744
TAT AAC AAT ATA CGA AGA AAT ACT AGC AGT AAT GGA TGC TTT TGG AGT Tyr Asn Asn Ile Arg Arg Asn Thr Ser Ser Asn Gly Cys Phe Trp Ser 1250 1255 1260	3792
TCT ATT TCT AAA GAG AAT GGA TGG AAA GAA TGA Ser Ile Ser Lys Glu Asn Gly Trp Lys Glu 1265 1270	3825

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1274 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- ii) MOLECULE TYPE: protein
- xi) SEQUENCE DESCRIPTION: SEO ID NO:71:

Met	Pro	Val	Ala	Ile	Asn	Ser	Phe	Asn	Tyr	Asn	Asp	Pro	Val	Asn	Asp
1				5					10					15	
Asp	Thr	Ile	Leu	Tyr	Met	Gln	Ile	Pro	Tyr	Glu	Glu	Lys	Ser	Lys	Lys
				20				25					30		
Tyr	Tyr	Lys	Ala	Phe	Glu	Ile	Met	Arg	Asn	Val	Trp	Ile	Ile	Pro	Glut
				35			40					45			
Arg	Asn	Thr	Ile	Gly	Thr	Asn	Pro	Ser	Asp	Phe	Asp	Pro	Pro	Ala	Ser
				50			55			60					

Leu Lys Asn Gly Ser Ser Ala Tyr Tyr Asp Pro Asn Tyr Leu Thr Thr  
 65 70 75 80  
 Asp Ala Glu Lys Asp Arg Tyr Leu Lys Thr Thr Ile Lys Leu Phe Lys  
 85 90 95  
 Arg Ile Asn Ser Asn Pro Ala Gly Lys Val Leu Leu Gln Glu Ile Ser  
 100 105 110  
 Tyr Ala Lys Pro Tyr Leu Gly Asn Asp His Thr Pro Ile Asp Glu Phe  
 115 120 125  
 Ser Pro Val Thr Arg Thr Thr Ser Val Asn Ile Lys Leu Ser Thr Asn  
 130 135 140  
 Val Glu Ser Ser Met Leu Leu Asn Leu Leu Val Leu Gly Ala Gly Pro  
 145 150 155 160  
 Asp Ile Phe Glu Ser Cys Cys Tyr Pro Val Arg Lys Leu Ile Asp Pro  
 165 170 175  
 Asp Val Val Tyr Asp Pro Ser Asn Tyr Gly Phe Gly Ser Ile Asn Ile  
 180 185 190  
 Val Thr Phe Ser Pro Glu Tyr Glu Tyr Thr Phe Asn Asp Ile Ser Gly  
 195 200 205  
 Gly His Asn Ser Ser Thr Glu Ser Phe Ile Ala Asp Pro Ala Ile Ser  
 210 215 220  
 Leu Ala His Glu Leu Ile His Ala Leu His Gly Leu Tyr Gly Ala Arg  
 225 230 235 240  
 Gly Val Thr Tyr Glu Glu Thr Ile Glu Val Lys Gln Ala Pro Leu Met  
 245 250 255  
 Ile Ala Glu Lys Pro Ile Arg Leu Glu Phe Leu Thr Phe Gly Gly  
 260 265 270  
 Gln Asp Leu Asn Ile Ile Thr Ser Ala Met Lys Glu Lys Ile Tyr Asn  
 275 280 285  
 Asn Leu Leu Ala Asn Tyr Glu Lys Ile Ala Thr Arg Leu Ser Glu Val  
 290 295 300  
 Asn Ser Ala Pro Pro Glu Tyr Asp Ile Asn Glu Tyr Lys Asp Tyr Phe  
 305 310 315 320  
 Gln Trp Lys Tyr Gly Leu Asp Lys Asn Ala Asp Gly Ser Tyr Thr Val  
 325 330 335  
 Asn Glu Asn Lys Phe Asn Glu Ile Tyr Lys Leu Tyr Ser Phe Thr  
 340 345 350  
 Glu Ser Asp Leu Ala Asn Lys Phe Lys Val Lys Cys Arg Asn Thr Tyr  
 355 360 365  
 Phe Ile Lys Tyr Glu Phe Leu Lys Val Pro Asn Leu Leu Asp Asp Asp  
 370 375 380  
 Ile Tyr Thr Val Ser Glu Gly Phe Asn Ile Gly Asn Leu Ala Val Asn  
 385 390 395 400

Asn Arg Gly Gln Ser Ile Lys Leu Asn Pro Lys Ile Ile Asp Ser Ile  
           405                                410                         415  
  
 Pro Asp Lys Gly Leu Val Glu Lys Ile Val Lys Phe Cys Lys Ser Val  
           420                                425                         430  
  
 Ile Pro Arg Lys Gly Thr Lys Ala Pro Pro Arg Leu Cys Ile Arg Val  
           435                                440                         445  
  
 Asn Asn Ser Glu Leu Phe Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu  
           450                                455                         460  
  
 Asn Asp Ile Asn Thr Pro Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn  
           465                                470                         475                         480  
  
 Asn Asn Tyr Arg Asn Asn Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser  
           485                                490                         495  
  
 Gln Thr Ile Pro Gln Ile Ser Asn Arg Thr Leu Asn Thr Leu Val Gln  
           500                                505                         510  
  
 Asp Asn Ser Tyr Val Pro Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile  
           515                                520                         525  
  
 Glu Glu Tyr Asp Val Val Asp Phe Asn Val Phe Phe Tyr Leu His Ala  
           530                                535                         540  
  
 Gln Lys Val Pro Glu Gly Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile  
           545                                550                         555                         560  
  
 Asp Thr Ala Leu Leu Glu Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu  
           565                                570                         575  
  
 Phe Ile Asp Thr Ile Asn Lys Pro Val Asn Ala Ala Leu Phe Ile Asp  
           580                                585                         590  
  
 Trp Ile Ser Lys Val Ile Arg Asp Phe Thr Thr Glu Ala Thr Gln Lys  
           595                                600                         605  
  
 Ser Thr Val Asp Lys Ile Ala Asp Ile Ser Leu Ile Val Pro Tyr Val  
           610                                615                         620  
  
 Gly Leu Ala Leu Asn Ile Ile Glu Ala Glu Lys Gly Asn Phe Glu  
           625                                630                         635                         640  
  
 Glu Ala Phe Glu Leu Leu Gly Val Gly Ile Leu Leu Glu Phe Val Pro  
           645                                650                         655  
  
 Glu Leu Thr Ile Pro Val Ile Leu Val Phe Thr Ile Lys Ser Tyr Ile  
           660                                665                         670  
  
 Asp Ser Tyr Glu Asn Lys Asn Lys Ala Ile Lys Ala Ile Asn Asn Ser  
           675                                680                         685  
  
 Leu Ile Glu Arg Glu Ala Lys Trp Lys Glu Ile Tyr Ser Trp Ile Val  
           690                                695                         700  
  
 Ser Asn Trp Leu Thr Arg Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu  
           705                                710                         715                         720  
  
 Gln Met Tyr Gln Ala Leu Gln Asn Gln Val Asp Ala Ile Lys Thr Ala  
           725                                730                         735

Ile Glu Tyr Lys Tyr Asn Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu  
 740 745 750

Glu Ser Glu Tyr Asn Ile Asn Asn Ile Glu Glu Glu Leu Asn Lys Lys  
 755 760 765

Val Ser Leu Ala Met Lys Asn Ile Glu Arg Phe Met Thr Glu Ser Ser  
 770 775 780

Ile Ser Tyr Leu Met Lys Leu Ile Asn Glu Ala Lys Val Gly Lys Leu  
 785 790 795 800

Lys Lys Tyr Asp Asn His Val Lys Ser Asp Leu Leu Asn Tyr Ile Leu  
 805 810 815

Asp His Arg Ser Ile Leu Gly Glu Gln Thr Asn Glu Leu Ser Asp Leu  
 820 825 830

Val Thr Ser Thr Leu Asn Ser Ser Ile Pro Phe Glu Leu Ser Ser Tyr  
 835 840 845

Thr Asn Asp Lys Ile Leu Ile Ile Tyr Phe Asn Arg Leu Tyr Lys Lys  
 850 855 860

Ile Lys Asp Ser Ser Ile Leu Asp Met Arg Tyr Glu Asn Asn Lys Phe  
 865 870 875 880

Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn Gly Asn Val  
 885 890 895

Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr Asn Ser Arg  
 900 905 910

Leu Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile Tyr Asn Ser  
 915 920 925

Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Lys His  
 930 935 940

Tyr Lys Pro Met Asn His Asn Arg Glu Tyr Thr Ile Ile Asn Cys Met  
 945 950 955 960

Gly Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Arg Thr Val Arg Asp  
 965 970 975

Cys Glu Ile Ile Trp Thr Leu Gln Asp Thr Ser Gly Asn Lys Glu Asn  
 980 985 990

Leu Ile Phe Arg Tyr Glu Glu Leu Asn Arg Ile Ser Asn Tyr Ile Asn  
 995 1000 1005

Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg  
 1010 1015 1020

Ile Tyr Ile Asn Gly Asn Leu Ile Val Glu Lys Ser Ile Ser Asn Leu  
 1025 1030 1035 1040

Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys  
 1045 1050 1055

Asp Asp Glu Thr Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asn Thr  
 1060 1065 1070

Glu Leu Asp Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asn Glu Pro Asp  
 1075 1080 1085  
 Pro Ser Ile Leu Lys Asn Tyr Trp Gly Asn Tyr Leu Leu Tyr Asn Lys  
 1090 1095 1100  
 Lys Tyr Tyr Leu Phe Asn Leu Leu Arg Lys Asp Lys Tyr Ile Thr Leu  
 1105 1110 1115 1120  
 Asn Ser Gly Ile Leu Asn Ile Asn Gln Gln Arg Gly Val Thr Glu Gly  
 1125 1130 1135  
 Ser Val Phe Leu Asn Tyr Lys Leu Tyr Glu Gly Val Glu Val Ile Ile  
 1140 1145 1150  
 Arg Lys Asn Gly Pro Ile Asp Ile Ser Asn Thr Asp Asn Phe Val Arg  
 1155 1160 1165  
 Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Gly Val Glu Tyr  
 1170 1175 1180  
 Arg Leu Tyr Ala Asp Thr Lys Ser Glu Lys Glu Lys Ile Ile Arg Thr  
 1185 1190 1195 1200  
 Ser Asn Leu Asn Asp Ser Leu Gly Gln Ile Ile Val Met Asp Ser Ile  
 1205 1210 1215  
 Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn Asn Gly Ser Asn Ile  
 1220 1225 1230  
 Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val Ala Ser Ser Trp Tyr  
 1235 1240 1245  
 Tyr Asn Asn Ile Arg Arg Asn Thr Ser Ser Asn Gly Cys Phe Trp Ser  
 1250 1255 1260  
 Ser Ile Ser Lys Glu Asn Gly Trp Lys Glu  
 1265 1270

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1460 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 108..1451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

AGATCTCGAT CCCGCGAAAT TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA	60
TTCCCTCTA GAAATAATTT TGTAACTT TAAGAAGGAG ATATACC ATG GGC CAT	116
	Met Gly His
	1

CAT CAT CAT CAT CAT CAT CAC AGC AGC GGC CAT ATC GAA GGT		164
His His His His His His His Ser Ser Gly His Ile Glu Gly		
5 10 15		
CGT CAT ATG GCT AGC ATG GCT ATT CTA ATT ATA TAT TTT AAT AGA TTA		212
Arg His Met Ala Ser Met Ala Ile Leu Ile Ile Tyr Phe Asn Arg Leu		
20 25 30 35		
TAT AAA AAA ATT AAA GAT AGT TCT ATT TTA GAT ATG CGA TAT GAA AAT		260
Tyr Lys Lys Ile Lys Asp Ser Ser Ile Leu Asp Met Arg Tyr Glu Asn		
40 45 50		
AAT AAA TTT ATA GAT ATC TCT GGA TAT GGT TCA AAT ATA AGC ATT AAT		308
Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn		
55 60 65		
GGA AAC GTA TAT ATT TAT TCA ACA AAT AGA AAT CAA TTT GGA ATA TAT		356
Gly Asn Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr		
70 75 80		
AAT AGT AGG CTT AGT GAA GTT AAT ATA GCT CAA AAT AAT GAT ATT ATA		404
Asn Ser Arg Leu Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile		
85 90 95		
TAC AAT AGT AGA TAT CAA AAT TTT AGT ATT AGT TTC TGG GTA AGG ATT		452
Tyr Asn Ser Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile		
100 105 110 115		
CCT AAA CAC TAC AAA CCT ATG AAT CAT AAT CGG GAA TAC ACT ATA ATA		500
Pro Lys His Tyr Lys Pro Met Asn His Asn Arg Glu Tyr Thr Ile Ile		
120 125 130		
AAT TGT ATG GGG AAT AAT TCG GGA TGG AAA ATA TCA CTT AGA ACT		548
Asn Cys Met Gly Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Arg Thr		
135 140 145		
GTT AGA GAT TGT GAA ATA ATT TGG ACT TTA CAA GAT ACT TCT GGA AAT		596
Val Arg Asp Cys Glu Ile Ile Trp Thr Leu Gln Asp Thr Ser Gly Asn		
150 155 160		
AAG GAA AAT TTA ATT TTT AGG TAT GAA GAA CTT AAT AGG ATA TCT AAT		644
Lys Glu Asn Leu Ile Phe Arg Tyr Glu Glu Leu Asn Arg Ile Ser Asn		
165 170 175		
TAT ATA AAT AAA TGG ATT TTT GTA ACT ATT ACT AAT AAT AGA TTA GGC		692
Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly		
180 185 190 195		
AAT TCT AGA ATT TAC ATC AAT GGA AAT TTA ATA GTT GAA AAA TCA ATT		740
Asn Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Val Glu Lys Ser Ile		
200 205 210		
TCG AAT TTA GGT GAT ATT CAT GTT AGT GAT AAT ATA TTA TTT AAA ATT		788
Ser Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile		
215 220 225		
GTT GGT TGT GAT GAT GAA ACG TAT GTT GGT ATA AGA TAT TTT AAA GTT		836
Val Gly Cys Asp Asp Glu Thr Tyr Val Gly Ile Arg Tyr Phe Lys Val		
230 235 240		

TTT AAT ACG GAA TTA GAT AAA ACA GAA ATT GAG ACT TTA TAT AGT AAT Phe Asn Thr Glu Leu Asp Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asn 245 250 255	884
GAG CCA GAT CCA AGT ATC TTA AAA AAC TAT TGG GGA AAT TAT TTG CTA Glu Pro Asp Pro Ser Ile Leu Lys Asn Tyr Trp Gly Asn Tyr Leu Leu 260 265 270 275	932
TAT AAT AAA AAA TAT TAT TTA TTC AAT TTA CTA AGA AAA GAT AAG TAT Tyr Asn Lys Lys Tyr Tyr Leu Phe Asn Leu Leu Arg Lys Asp Lys Tyr 280 285 290	980
ATT ACT CTG AAT TCA GGC ATT TTA AAT ATT AAT CAA CAA AGA GGT GTT Ile Thr Leu Asn Ser Gly Ile Leu Asn Ile Asn Gln Gln Arg Gly Val 295 300 305	1028
ACT GAA GGC TCT GTT TTT TTG AAC TAT AAA TTA TAT GAA GGA GTA GAA Thr Glu Gly Ser Val Phe Leu Asn Tyr Lys Leu Tyr Glu Gly Val Glu 310 315 320	1076
GTC ATT ATA AGA AAA AAT GGT CCT ATA GAT ATA TCT AAT ACA GAT AAT Val Ile Ile Arg Lys Asn Gly Pro Ile Asp Ile Ser Asn Thr Asp Asn 325 330 335	1124
TTT GTT AGA AAA AAC GAT CTA GCA TAC ATT AAT GTA GTA GAT CGT GGT Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Gly 340 345 350 355	1172
GTA GAA TAT CGG TTA TAT GCT GAT ACA AAA TCA GAG AAA GAG AAA ATA Val Glu Tyr Arg Leu Tyr Ala Asp Thr Lys Ser Glu Lys Glu Lys Ile 360 365 370	1220
ATA AGA ACA TCT AAT CTA AAC GAT AGC TTA GGT CAA ATT ATA GTT ATG Ile Arg Thr Ser Asn Leu Asn Asp Ser Leu Gly Gln Ile Ile Val Met 375 380 385	1268
GAT TCA ATA GGA AAT AAT TGC ACA ATG AAT TTT CAA AAC AAT AAT GGG Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn Asn Gly 390 395 400	1316
AGC AAT ATA GGA TTA CTA GGT TTT CAT TCA AAT AAT TTG GTT GCT AGT Ser Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val Ala Ser 405 410 415	1364
AGT TGG TAT TAT AAC AAT ATA CGA AGA AAT ACT AGC AGT AAT GGA TGC Ser Trp Tyr Tyr Asn Asn Ile Arg Arg Asn Thr Ser Ser Asn Gly Cys 420 425 430 435	1412
TTT TGG AGT TCT ATT TCT AAA GAG AAT GGA TGG AAA GAA TGAAAGCTT Phe Trp Ser Ser Ile Ser Lys Glu Asn Gly Trp Lys Glu 440 445	1460

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 448 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met Gly His His His His His His His His His Ser Ser Gly His  
1 5 10 15

Ile Glu Gly Arg His Met Ala Ser Met Ala Ile Leu Ile Ile Tyr Phe  
20 25 30

Asn Arg Leu Tyr Lys Lys Ile Lys Asp Ser Ser Ile Leu Asp Met Arg  
35 40 45

Tyr Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile  
50 55 60

Ser Ile Asn Gly Asn Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe  
65 70 75 80

Gly Ile Tyr Asn Ser Arg Leu Ser Glu Val Asn Ile Ala Gln Asn Asn  
85 90 95

Asp Ile Ile Tyr Asn Ser Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp  
100 105 110

Val Arg Ile Pro Lys His Tyr Lys Pro Met Asn His Asn Arg Glu Tyr  
115 120 125

Thr Ile Ile Asn Cys Met Gly Asn Asn Asn Ser Gly Trp Lys Ile Ser  
130 135 140

Leu Arg Thr Val Arg Asp Cys Glu Ile Ile Trp Thr Leu Gln Asp Thr  
145 150 155 160

Ser Gly Asn Lys Glu Asn Leu Ile Phe Arg Tyr Glu Glu Leu Asn Arg  
165 170 175

Ile Ser Asn Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn  
180 185 190

Arg Leu Gly Asn Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Val Glu  
195 200 205

Lys Ser Ile Ser Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu  
210 215 220

Phe Lys Ile Val Gly Cys Asp Asp Glu Thr Tyr Val Gly Ile Arg Tyr  
225 230 235 240

Phe Lys Val Phe Asn Thr Glu Leu Asp Lys Thr Glu Ile Glu Thr Leu  
245 250 255

Tyr Ser Asn Glu Pro Asp Pro Ser Ile Leu Lys Asn Tyr Trp Gly Asn  
260 265 270

Tyr Leu Leu Tyr Asn Lys Tyr Tyr Leu Phe Asn Leu Leu Arg Lys  
275 280 285

Asp Lys Tyr Ile Thr Leu Asn Ser Gly Ile Leu Asn Ile Asn Gln Gln  
290 295 300

Arg Gly Val Thr Glu Gly Ser Val Phe Leu Asn Tyr Lys Leu Tyr Glu  
305 310 315 320

Gly Val Glu Val Ile Ile Arg Lys Asn Gly Pro Ile Asp Ile Ser Asn  
                   325                  330                  335  
 Thr Asp Asn Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val  
                   340                  345                  350  
 Asp Arg Gly Val Glu Tyr Arg Leu Tyr Ala Asp Thr Lys Ser Glu Lys  
                   355                  360                  365  
 Glu Lys Ile Ile Arg Thr Ser Asn Leu Asn Asp Ser Leu Gly Gln Ile  
                   370                  375                  380  
 Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn  
                   385                  390                  395                  400  
 Asn Asn Gly Ser Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu  
                   405                  410                  415  
 Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Arg Asn Thr Ser Ser  
                   420                  425                  430  
 Asn Gly Cys Phe Trp Ser Ser Ile Ser Lys Glu Asn Gly Trp Lys Glu  
                   435                  440                  445

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CGCCATGGCT ATTCTAACCA TATATTTAA TAG

33

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GCAAGCTTTC ATTCTTTCCA TCCATTCTC

29

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ATG CCA GTT AAT ATA AAA AAC TTT AAT TAT AAT GAC CCT ATT AAT AAT Met Pro Val Asn Ile Lys Asn Phe Asn Tyr Asn Asp Pro Ile Asn Asn 1 5 10 15	48
GAT GAC ATT ATT ATG ATG GAA CCA TTC AAT GAC CCA GGG CCA GGA ACA Asp Asp Ile Ile Met Met Glu Pro Phe Asn Asp Pro Gly Pro Gly Thr 20 25 30	96
TAT TAT AAA GCT TTT AGG ATT ATA GAT CGT ATT TGG ATA GTA CCA GAA Tyr Tyr Lys Ala Phe Arg Ile Ile Asp Arg Ile Trp Ile Val Pro Glu 35 40 45	144
AGG TTT ACT TAT GGA TTT CAA CCT GAC CAA TTT AAT GCC AGT ACA GGA Arg Phe Thr Tyr Gly Phe Gln Pro Asp Gln Phe Asn Ala Ser Thr Gly 50 55 60	192
GTT TTT AGT AAA GAT GTC TAC GAA TAT TAC GAT CCA ACT TAT TTA AAA Val Phe Ser Lys Asp Val Tyr Glu Tyr Tyr Asp Pro Thr Tyr Leu Lys 65 70 75 80	240
ACC GAT GCT GAA AAA GAT AAA TTT TTA AAA ACA ATG ATT AAA TTA TTT Thr Asp Ala Glu Lys Asp Lys Phe Leu Lys Thr Met Ile Lys Leu Phe 85 90 95	288
AAT AGA ATT AAT TCA AAA CCA TCA GGA CAG AGA TTA CTG GAT ATG ATA Asn Arg Ile Asn Ser Lys Pro Ser Gly Gln Arg Leu Leu Asp Met Ile 100 105 110	336
GTA GAT GCT ATA CCT TAT CTT GGA AAT GCA TCT ACA CCC GAC AAA Val Asp Ala Ile Pro Tyr Leu Gly Asn Ala Ser Thr Pro Pro Asp Lys 115 120 125	384
TTT GCA GCA AAT GTT GCA AAT GTC TCT ATT AAT AAA AAA ATT ATC CAA Phe Ala Ala Asn Val Ala Asn Val Ser Ile Asn Lys Lys Ile Ile Gln 130 135 140	432
CCT GGA GCT GAA GAT CAA ATA AAA GGT TTA ATG ACA AAT TTA ATA ATA Pro Gly Ala Glu Asp Gln Ile Lys Gly Leu Met Thr Asn Leu Ile Ile 145 150 155 160	480
TTT GGA CCA GGA CCA GTT CTA AGT GAT AAT TTT ACT GAT AGT ATG ATT Phe Gly Pro Gly Pro Val Leu Ser Asp Asn Phe Thr Asp Ser Met Ile 165 170 175	528

ATG AAT GGC CAT TCC CCA ATA TCA GAA GGA TTT GGT GCA AGA ATG ATG Met Asn Gly His Ser Pro Ile Ser Glu Gly Phe Gly Ala Arg Met Met	576
180 185 190	
ATA AGA TTT TGT CCT AGT TGT TTA AAT GTA TTT AAT AAT GTT CAG GAA Ile Arg Phe Cys Pro Ser Cys Leu Asn Val Phe Asn Asn Val Gln Glu	624
195 200 205	
AAT AAA GAT ACA TCT ATA TTT AGT AGA CGC GCG TAT TTT GCA GAT CCA Asn Lys Asp Thr Ser Ile Phe Ser Arg Arg Ala Tyr Phe Ala Asp Pro	672
210 215 220	
GCT CTA ACG TTA ATG CAT GAA CTT ATA CAT GTG TTA CAT GGA TTA TAT Ala Leu Thr Leu Met His Glu Leu Ile His Val Leu His Gly Leu Tyr	720
225 230 235 240	
GGA ATT AAG ATA AGT AAT TTA CCA ATT ACT CCA AAT ACA AAA GAA TTT Gly Ile Lys Ile Ser Asn Leu Pro Ile Thr Pro Asn Thr Lys Glu Phe	768
245 250 255	
TTC ATG CAA CAT AGC GAT CCT GTA CAA GCA GAA GAA CTA TAT ACA TTC Phe Met Gln His Ser Asp Pro Val Gln Ala Glu Glu Leu Tyr Thr Phe	816
260 265 270	
GGA GGA CAT GAT CCT AGT GTT ATA AGT CCT TCT ACG GAT ATG AAT ATT Gly Gly His Asp Pro Ser Val Ile Ser Pro Ser Thr Asp Met Asn Ile	864
275 280 285	
TAT AAT AAA GCG TTA CAA AAT TTT CAA GAT ATA GCT AAT AGG CTT AAT Tyr Asn Lys Ala Leu Gln Asn Phe Gln Asp Ile Ala Asn Arg Leu Asn	912
290 295 300	
ATT GTT TCA AGT GCC CAA GGG AGT GGA ATT GAT ATT TCC TTA TAT AAA Ile Val Ser Ser Ala Gln Gly Ser Gly Ile Asp Ile Ser Leu Tyr Lys	960
305 310 315 320	
CAA ATA TAT AAA AAT AAA TAT GAT TTT GTT GAA GAT CCT AAT GGA AAA Gln Ile Tyr Lys Asn Lys Tyr Asp Phe Val Glu Asp Pro Asn Gly Lys	1008
325 330 335	
TAT AGT GTA GAT AAG GAT AAG TTT GAT AAA TTA TAT AAG GCC TTA ATG Tyr Ser Val Asp Lys Asp Lys Phe Asp Lys Leu Tyr Lys Ala Leu Met	1056
340 345 350	
TTT GGC TTT ACT GAA ACT AAT CTA GCT GGT GAA TAT GGA ATA AAA ACT Phe Gly Phe Thr Glu Thr Asn Leu Ala Gly Glu Tyr Gly Ile Lys Thr	1104
355 360 365	
AGG TAT TCT TAT TTT AGT GAA TAT TTG CCA CCG ATA AAA ACT GAA AAA Arg Tyr Ser Tyr Phe Ser Glu Tyr Leu Pro Pro Ile Lys Thr Glu Lys	1152
370 375 380	
TTG TTA GAC AAT ACA ATT TAT ACT CAA AAT GAA GGC TTT AAC ATA GCT Leu Leu Asp Asn Thr Ile Tyr Thr Gln Asn Glu Gly Phe Asn Ile Ala	1200
385 390 395 400	
AGT AAA AAT CTC AAA ACG GAA TTT AAT GGT CAG AAT AAG GCG GTA AAT Ser Lys Asn Leu Lys Thr Glu Phe Asn Gly Gln Asn Lys Ala Val Asn	1248
405 410 415	

AAA GAG GCT TAT GAA GAA ATC AGC CTA GAA CAT CTC GTT ATA TAT AGA		1296
Lys Glu Ala Tyr Glu Glu Ile Ser Leu Glu His Leu Val Ile Tyr Arg		
420	425	430
ATA GCA ATG TGC AAG CCT GTA ATG TAC AAA AAT ACC GGT AAA TCT GAA		1344
Ile Ala Met Cys Lys Pro Val Met Tyr Lys Asn Thr Gly Lys Ser Glu		
435	440	445
CAG TGT ATT ATT GTT AAT AAT GAG GAT TTA TTT TTC ATA GCT AAT AAA		1392
Gln Cys Ile Ile Val Asn Asn Glu Asp Leu Phe Phe Ile Ala Asn Lys		
450	455	460
GAT AGT TTT TCA AAA GAT TTA GCT AAA GCA GAA ACT ATA GCA TAT AAT		1440
Asp Ser Phe Ser Lys Asp Leu Ala Lys Ala Glu Thr Ile Ala Tyr Asn		
465	470	475
ACA CAA AAT AAT ACT ATA GAA AAT AAT TTT TCT ATA GAT CAG TTG ATT		1488
Thr Gln Asn Asn Thr Ile Glu Asn Asn Phe Ser Ile Asp Gln Leu Ile		
485	490	495
TTA GAT AAT GAT TTA AGC AGT GGC ATA GAC TTA CCA AAT GAA AAC ACA		1536
Leu Asp Asn Asp Leu Ser Ser Gly Ile Asp Leu Pro Asn Glu Asn Thr		
500	505	510
GAA CCA TTT ACA AAT TTT GAC GAC ATA GAT ATC CCT GTG TAT ATT AAA		1584
Glu Pro Phe Thr Asn Phe Asp Asp Ile Asp Ile Pro Val Tyr Ile Lys		
515	520	525
CAA TCT GCT TTA AAA AAA ATT TTT GTG GAT GGA GAT AGC CTT TTT GAA		1632
Gln Ser Ala Leu Lys Lys Ile Phe Val Asp Gly Asp Ser Leu Phe Glu		
530	535	540
TAT TTA CAT GCT CAA ACA TTT CCT TCT AAT ATA GAA AAT CTA CAA CTA		1680
Tyr Leu His Ala Gln Thr Phe Pro Ser Asn Ile Glu Asn Leu Gln Leu		
545	550	555
560		
ACG AAT TCA TTA AAT GAT GCT TTA AGA AAT AAT AAA GTC TAT ACT		1728
Thr Asn Ser Leu Asn Asp Ala Leu Arg Asn Asn Asn Lys Val Tyr Thr		
565	570	575
TTT TTT TCT ACA AAC CTT GTT GAA AAA GCT AAT ACA GTT GTA GGT GCT		1776
Phe Phe Ser Thr Asn Leu Val Glu Lys Ala Asn Thr Val Val Gly Ala		
580	585	590
TCA CTT TTT GTA AAC TGG GTA AAA GGA GTA ATA GAT GAT TTT ACA TCT		1824
Ser Leu Phe Val Asn Trp Val Lys Gly Val Ile Asp Asp Phe Thr Ser		
595	600	605
GAA TCC ACA CAA AAA AGT ACT ATA GAT AAA GTT TCA GAT GTA TCC ATA		1872
Glu Ser Thr Gln Lys Ser Thr Ile Asp Lys Val Ser Asp Val Ser Ile		
610	615	620
ATT ATT CCC TAT ATA GGA CCT GCT TTG AAT GTA GGA AAT GAA ACA GCT		1920
Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Val Gly Asn Glu Thr Ala		
625	630	635
640		
AAA GAA AAT TTT AAA AAT GCT TTT GAA ATA GGT GGA GCC GCT ATC TTA		1968
Lys Glu Asn Phe Lys Asn Ala Phe Glu Ile Gly Gly Ala Ala Ile Leu		
645	650	655

ATG GAG TTT ATT CCA GAA CTT ATT GTA CCT ATA GTT GGA TTT TTT ACA Met Glu Phe Ile Pro Glu Leu Ile Val Pro Ile Val Gly Phe Phe Thr 660 665 670	2016
TTA GAA TCA TAT GTA GGA AAT AAA GGG CAT ATT ATT ATG ACG ATA TCC Leu Glu Ser Tyr Val Gly Asn Lys Gly His Ile Ile Met Thr Ile Ser 675 680 685	2064
AAT GCT TTA AAG AAA AGG GAT CAA AAA TGG ACA GAT ATG TAT GGT TTG Asn Ala Leu Lys Lys Arg Asp Gln Lys Trp Thr Asp Met Tyr Gly Leu 690 695 700	2112
ATA GTA TCG CAG TGG CTC TCA ACG GTT AAT ACT CAA TTT TAT ACA ATA Ile Val Ser Gln Trp Leu Ser Thr Val Asn Thr Gln Phe Tyr Thr Ile 705 710 715 720	2160
AAA GAA AGA ATG TAC AAT GCT TTA AAT AAT CAA TCA CAA GCA ATA GAA Lys Glu Arg Met Tyr Asn Ala Leu Asn Asn Gln Ser Gln Ala Ile Glu 725 730 735	2208
AAA ATA ATA GAA GAT CAA TAT AAT AGA TAT AGT GAA GAA GAT AAA ATG Lys Ile Ile Glu Asp Gln Tyr Asn Arg Tyr Ser Glu Glu Asp Lys Met 740 745 750	2256
AAT ATT AAC ATT GAT TTT AAT GAT ATA GAT TTT AAA CTT AAT CAA AGT Asn Ile Asn Ile Asp Phe Asn Asp Ile Asp Phe Lys Leu Asn Gln Ser 755 760 765	2304
ATA AAT TTA GCA ATA AAC AAT ATA GAT GAT TTT ATA AAC CAA TGT TCT Ile Asn Leu Ala Ile Asn Asn Ile Asp Asp Phe Ile Asn Gln Cys Ser 770 775 780	2352
ATA TCA TAT CTA ATG AAT AGA ATG ATT CCA TTA GCT GTA AAA AAG TTA Ile Ser Tyr Leu Met Asn Arg Met Ile Pro Leu Ala Val Lys Lys Leu 785 790 795 800	2400
AAA GAC TTT GAT GAT AAT CTT AAG AGA GAT TTA TTG GAG TAT ATA GAT Lys Asp Phe Asp Asp Asn Leu Lys Arg Asp Leu Leu Glu Tyr Ile Asp 805 810 815	2448
ACA AAT GAA CTA TAT TTA CTT GAT GAA GTA AAT ATT CTA AAA TCA AAA Thr Asn Glu Leu Tyr Leu Leu Asp Glu Val Asn Ile Leu Lys Ser Lys 820 825 830	2496
GTA AAT AGA CAC CTA AAA GAC AGT ATA CCA TTT GAT CTT TCA CTA TAT Val Asn Arg His Leu Lys Asp Ser Ile Pro Phe Asp Leu Ser Leu Tyr 835 840 845	2544
ACC AAG GAC ACA ATT TTA ATA CAA GTT TTT AAT AAT TAT ATT AGT AAT Thr Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile Ser Asn 850 855 860	2592
ATT AGT AGT AAT GCT ATT TTA AGT TTA AGT TAT AGA GGT GGG CGT TTA Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly Arg Leu 865 870 875 880	2640
ATA GAT TCA TCT GGA TAT GGT GCA ACT ATG AAT GTA GGT TCA GAT GTT Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser Asp Val 885 890 895	2688

ATC TTT AAT GAT ATA GGA AAT GGT CAA TTT AAA TTA AAT AAT TCT GAA Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn Ser Glu 900 905 910	2736
AAT AGT AAT ATT ACG GCA CAT CAA AGT AAA TTC GTT GTA TAT GAT AGT Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr Asp Ser 915 920 925	2784
ATG TTT GAT AAT TTT AGC ATT AAC TTT TGG GTA AGG ACT CCT AAA TAT Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro Lys Tyr 930 935 940	2832
AAT AAT AAT GAT ATA CAA ACT TAT CTT CAA AAT GAG TAT ACA ATA ATT Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr Ile Ile 945 950 955 960	2880
AGT TGT ATA AAA AAT GAC TCA GGA TGG AAA GTA TCT ATT AAG GGA AAT Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys Gly Asn 965 970 975	2928
AGA ATA ATA TGG ACA TTA ATA GAT GTT AAT GCA AAA TCT AAA TCA ATA Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys Ser Ile 980 985 990	2976
TTT TTC GAA TAT AGT ATA AAA GAT AAT ATA TCA GAT TAT ATA AAT AAA Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile Asn Lys 995 1000 1005	3024
TGG TTT TCC ATA ACT ATT ACT AAT GAT AGA TTA GGT AAC GCA AAT ATT Trp Phe Ser Ile Thr Ile Asn Asp Arg Leu Gly Asn Ala Asn Ile 1010 1015 1020	3072
TAT ATA AAT GGA AGT TTG AAA AAA AGT GAA AAA ATT TTA AAC TTA GAT Tyr Ile Asn Gly Ser Leu Lys Ser Glu Lys Ile Leu Asn Leu Asp 1025 1030 1035 1040	3120
AGA ATT AAT TCT AGT AAT GAT ATA GAC TTC AAA TTA ATT AAT TGT ACA Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn Cys Thr 1045 1050 1055	3168
GAT ACT ACT AAA TTT GTT TGG ATT AAG GAT TTT AAT ATT TTT GGT AGA Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe Gly Arg 1060 1065 1070	3216
GAA TTA AAT GCT ACA GAA GTA TCT TCA CTA TAT TGG ATT CAA TCA TCT Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln Ser Ser 1075 1080 1085	3264
ACA AAT ACT TTA AAA GAT TTT TGG GGG AAT CCT TTA AGA TAC GAT ACA Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr 1090 1095 1100	3312
CAA TAC TAT CTG TTT AAT CAA GGT ATG CAA AAT ATC TAT ATA AAG TAT Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile Lys Tyr 1105 1110 1115 1120	3360
TTT AGT AAA GCT TCT ATG GGG GAA ACT GCA CCA CGT ACA AAC TTT AAT Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn Phe Asn 1125 1130 1135	3408

AAT GCA GCA ATA AAT TAT CAA AAT TTA TAT CTT GGT TTA CGA TTT ATT Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg Phe Ile 1140 1145 1150	3456
ATA AAA AAA GCA TCA AAT TCT CGG AAT ATA AAT AAT GAT AAT ATA GTC Ile Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn Ile Val 1155 1160 1165	3504
AGA GAA GGA GAT TAT ATA TAT CTT AAT ATT GAT AAT ATT TCT GAT GAA Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser Asp Glu 1170 1175 1180	3552
TCT TAC AGA GTA TAT GTT TTG GTG AAT TCT AAA GAA ATT CAA ACT CAA Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln Thr Gln 1185 1190 1195 1200	3600
TTA TTT TTA GCA CCC ATA AAT GAT GAT CCT ACG TTC TAT GAT GTA CTA Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp Val Leu 1205 1210 1215	3648
CAA ATA AAA AAA TAT TAT GAA AAA ACA ACA TAT AAT TGT CAG ATA CTT Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln Ile Leu 1220 1225 1230	3696
TGC GAA AAA GAT ACT AAA ACA TTT GGG CTG TTT GGA ATT GGT AAA TTT Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe Gly Ile Gly Lys Phe 1235 1240 1245	3744
GTT AAA GAT TAT GGA TAT GTT TGG GAT ACC TAT GAT AAT TAT TTT TGC Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr Asp Asn Tyr Phe Cys 1250 1255 1260	3792
ATA AGT CAG TGG TAT CTC AGA AGA ATA TCT GAA AAT ATA AAT AAA TTA Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn Lys Leu 1265 1270 1275 1280	3840
AGG TTG GGA TGT AAT TGG CAA TTC ATT CCC GTG GAT GAA GGA TGG ACA Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly Trp Thr 1285 1290 1295	3888
GAA TAA Glu	3894

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1297 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Pro Val Asn Ile Lys Asn Phe Asn Tyr Asn Asp Pro Ile Asn Asn 1 5 10 15
Asp Asp Ile Ile Met Met Glu Pro Phe Asn Asp Pro Gly Pro Gly Thr 20 25 30
Tyr Tyr Lys Ala Phe Arg Ile Ile Asp Arg Ile Trp Ile Val Pro Glu 35 40 45

Arg Phe Thr Tyr Gly Phe Gln Pro Asp Gln Phe Asn Ala Ser Thr Gly  
 50 55 60

Val Phe Ser Lys Asp Val Tyr Glu Tyr Tyr Asp Pro Thr Tyr Leu Lys  
 65 70 75 80

Thr Asp Ala Glu Lys Asp Lys Phe Leu Lys Thr Met Ile Lys Leu Phe  
 85 90 95

Asn Arg Ile Asn Ser Lys Pro Ser Gly Gln Arg Leu Leu Asp Met Ile  
 100 105 110

Val Asp Ala Ile Pro Tyr Leu Gly Asn Ala Ser Thr Pro Pro Asp Lys  
 115 120 125

Phe Ala Ala Asn Val Ala Asn Val Ser Ile Asn Lys Lys Ile Ile Gln  
 130 135 140

Pro Gly Ala Glu Asp Gln Ile Lys Gly Leu Met Thr Asn Leu Ile Ile  
 145 150 155 160

Phe Gly Pro Gly Pro Val Leu Ser Asp Asn Phe Thr Asp Ser Met Ile  
 165 170 175

Met Asn Gly His Ser Pro Ile Ser Glu Gly Phe Gly Ala Arg Met Met  
 180 185 190

Ile Arg Phe Cys Pro Ser Cys Leu Asn Val Phe Asn Asn Val Gln Glu  
 195 200 205

Asn Lys Asp Thr Ser Ile Phe Ser Arg Arg Ala Tyr Phe Ala Asp Pro  
 210 215 220

Ala Leu Thr Leu Met His Glu Leu Ile His Val Leu His Gly Leu Tyr  
 225 230 235 240

Gly Ile Lys Ile Ser Asn Leu Pro Ile Thr Pro Asn Thr Lys Glu Phe  
 245 250 255

Phe Met Gln His Ser Asp Pro Val Gln Ala Glu Glu Leu Tyr Thr Phe  
 260 265 270

Gly Gly His Asp Pro Ser Val Ile Ser Pro Ser Thr Asp Met Asn Ile  
 275 280 285

Tyr Asn Lys Ala Leu Gln Asn Phe Gln Asp Ile Ala Asn Arg Leu Asn  
 290 295 300

Ile Val Ser Ser Ala Gln Gly Ser Gly Ile Asp Ile Ser Leu Tyr Lys  
 305 310 315 320

Gln Ile Tyr Lys Asn Lys Tyr Asp Phe Val Glu Asp Pro Asn Gly Lys  
 325 330 335

Tyr Ser Val Asp Lys Asp Lys Phe Asp Lys Leu Tyr Lys Ala Leu Met  
 340 345 350

Phe Gly Phe Thr Glu Thr Asn Leu Ala Gly Glu Tyr Gly Ile Lys Thr  
 355 360 365

Arg Tyr Ser Tyr Phe Ser Glu Tyr Leu Pro Pro Ile Lys Thr Glu Lys  
 370 375 380

Leu Leu Asp Asn Thr Ile Tyr Thr Gln Asn Glu Gly Phe Asn Ile Ala  
 385 390 395 400  
 Ser Lys Asn Leu Lys Thr Glu Phe Asn Gly Gln Asn Lys Ala Val Asn  
 405 410 415  
 Lys Glu Ala Tyr Glu Glu Ile Ser Leu Glu His Leu Val Ile Tyr Arg  
 420 425 430  
 Ile Ala Met Cys Lys Pro Val Met Tyr Lys Asn Thr Gly Lys Ser Glu  
 435 440 445  
 Gln Cys Ile Ile Val Asn Asn Glu Asp Leu Phe Phe Ile Ala Asn Lys  
 450 455 460  
 Asp Ser Phe Ser Lys Asp Leu Ala Lys Ala Glu Thr Ile Ala Tyr Asn  
 465 470 475 480  
 Thr Gln Asn Asn Thr Ile Glu Asn Asn Phe Ser Ile Asp Gln Leu Ile  
 485 490 495  
 Leu Asp Asn Asp Leu Ser Ser Gly Ile Asp Leu Pro Asn Glu Asn Thr  
 500 505 510  
 Glu Pro Phe Thr Asn Phe Asp Asp Ile Asp Ile Pro Val Tyr Ile Lys  
 515 520 525  
 Gln Ser Ala Leu Lys Lys Ile Phe Val Asp Gly Asp Ser Leu Phe Glu  
 530 535 540  
 Tyr Leu His Ala Gln Thr Phe Pro Ser Asn Ile Glu Asn Leu Gln Leu  
 545 550 555 560  
 Thr Asn Ser Leu Asn Asp Ala Leu Arg Asn Asn Asn Lys Val Tyr Thr  
 565 570 575  
 Phe Phe Ser Thr Asn Leu Val Glu Lys Ala Asn Thr Val Val Gly Ala  
 580 585 590  
 Ser Leu Phe Val Asn Trp Val Lys Gly Val Ile Asp Asp Phe Thr Ser  
 595 600 605  
 Glu Ser Thr Gln Lys Ser Thr Ile Asp Lys Val Ser Asp Val Ser Ile  
 610 615 620  
 Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Val Gly Asn Glu Thr Ala  
 625 630 635 640  
 Lys Glu Asn Phe Lys Asn Ala Phe Glu Ile Gly Gly Ala Ala Ile Leu  
 645 650 655  
 Met Glu Phe Ile Pro Glu Leu Ile Val Pro Ile Val Gly Phe Phe Thr  
 660 665 670  
 Leu Glu Ser Tyr Val Gly Asn Lys Gly His Ile Ile Met Thr Ile Ser  
 675 680 685  
 Asn Ala Leu Lys Lys Arg Asp Gln Lys Trp Thr Asp Met Tyr Gly Leu  
 690 695 700  
 Ile Val Ser Gln Trp Leu Ser Thr Val Asn Thr Gln Phe Tyr Thr Ile  
 705 710 715 720

Lys Glu Arg Met Tyr Asn Ala Leu Asn Asn Gln Ser Gln Ala Ile Glu  
 725 730 735  
 Lys Ile Ile Glu Asp Gln Tyr Asn Arg Tyr Ser Glu Glu Asp Lys Met  
 740 745 750  
 Asn Ile Asn Ile Asp Phe Asn Asp Ile Asp Phe Lys Leu Asn Gln Ser  
 755 760 765  
 Ile Asn Leu Ala Ile Asn Asn Ile Asp Asp Phe Ile Asn Gln Cys Ser  
 770 775 780  
 Ile Ser Tyr Leu Met Asn Arg Met Ile Pro Leu Ala Val Lys Lys Leu  
 785 790 795 800  
 Lys Asp Phe Asp Asp Asn Leu Lys Arg Asp Leu Leu Glu Tyr Ile Asp  
 805 810 815  
 Thr Asn Glu Leu Tyr Leu Leu Asp Glu Val Asn Ile Leu Lys Ser Lys  
 820 825 830  
 Val Asn Arg His Leu Lys Asp Ser Ile Pro Phe Asp Leu Ser Leu Tyr  
 835 840 845  
 Thr Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile Ser Asn  
 850 855 860  
 Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly Arg Leu  
 865 870 875 880  
 Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser Asp Val  
 885 890 895  
 Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn Ser Glu  
 900 905 910  
 Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr Asp Ser  
 915 920 925  
 Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro Lys Tyr  
 930 935 940  
 Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr Ile Ile  
 945 950 955 960  
 Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys Gly Asn  
 965 970 975  
 Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys Ser Ile  
 980 985 990  
 Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile Asn Lys  
 995 1000 1005  
 Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala Asn Ile  
 1010 1015 1020  
 Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn Leu Asp  
 1025 1030 1035 1040  
 Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn Cys Thr  
 1045 1050 1055

Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe Gly Arg  
 1060 1065 1070  
 Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln Ser Ser  
 1075 1080 1085  
 Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr  
 1090 1095 1100  
 Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile Lys Tyr  
 1105 1110 1115 1120  
 Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn Phe Asn  
 1125 1130 1135  
 Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg Phe Ile  
 1140 1145 1150  
 Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn Ile Val  
 1155 1160 1165  
 Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser Asp Glu  
 1170 1175 1180  
 Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln Thr Gln  
 1185 1190 1195 1200  
 Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp Val Leu  
 1205 1210 1215  
 Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln Ile Leu  
 1220 1225 1230  
 Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe Gly Ile Gly Lys Phe  
 1235 1240 1245  
 Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr Asp Asn Tyr Phe Cys  
 1250 1255 1260  
 Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn Lys Leu  
 1265 1270 1275 1280  
 Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly Trp Thr  
 1285 1290 1295

Glu

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1535 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 108..1526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

AGATCTCGAT CCCGCGAAAT TAATACGACT CACTATAGGG GAATTGTGAG CGGATAACAA	60
TTCCCCTCTA GAAATAATTT TGTAACTT TAAGAAGGAG ATATACC ATG GGC CAT Met Gly His	116 1
CAT CAT CAT CAT CAT CAT CAC AGC AGC GGC CAT ATC GAA GGT His His His His His His Ser Ser Gly His Ile Glu Gly	164 5                   10               15
CGT CAT ATG GCT AGC ATG GCT GAC ACA ATT TTA ATA CAA GTT TTT AAT Arg His Met Ala Ser Met Ala Asp Thr Ile Leu Ile Gln Val Phe Asn	212 20               25               30               35
AAT TAT ATT AGT AAT ATT AGT AAT GCT ATT TTA AGT TTA AGT TAT Asn Tyr Ile Ser Asn Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr	260 40               45               50
AGA GGT GGG CGT TTA ATA GAT TCA TCT GGA TAT GGT GCA ACT ATG AAT Arg Gly Arg Leu Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn	308 55               60               65
GTA GGT TCA GAT GTT ATC TTT AAT GAT ATA GGA AAT GGT CAA TTT AAA Val Gly Ser Asp Val Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys	356 70               75               80
TTA AAT AAT TCT GAA AAT AGT AAT ATT ACG GCA CAT CAA AGT AAA TTC Leu Asn Asn Ser Glu Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe	404 85               90               95
GTT GTA TAT GAT ATG TTT GAT AAT TTT AGC ATT AAC TTT TGG GTA Val Val Tyr Asp Ser Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val	452 100              105              110              115
AGG ACT CCT AAA TAT AAT AAT GAT ATA CAA ACT TAT CTT CAA AAT Arg Thr Pro Lys Tyr Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn	500 120              125              130
GAG TAT ACA ATA ATT AGT TGT ATA AAA AAT GAC TCA GGA TGG AAA GTA Glu Tyr Thr Ile Ile Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val	548 135              140              145
TCT ATT AAG GGA AAT AGA ATA ATA TGG ACA TTA ATA GAT GTT AAT GCA Ser Ile Lys Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala	596 150              155              160
AAA TCT AAA TCA ATA TTT TTC GAA TAT AGT ATA AAA GAT AAT ATA TCA Lys Ser Lys Ser Ile Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser	644 165              170              175
GAT TAT ATA AAT AAA TGG TTT TCC ATA ACT ATT ACT AAT GAT AGA TTA Asp Tyr Ile Asn Lys Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu	692 180              185              190              195
GGT AAC GCA AAT ATT TAT ATA AAT GGA AGT TTG AAA AAA AGT GAA AAA Gly Asn Ala Asn Ile Tyr Ile Asn Gly Ser Leu Lys Ser Glu Lys	740 200              205              210

ATT TTA AAC TTA GAT AGA ATT AAT TCT AGT AAT GAT ATA GAC TTC AAA Ile Leu Asn Leu Asp Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys 215 220 225	788
TTA ATT AAT TGT ACA GAT ACT ACT AAA TTT GTT TGG ATT AAG GAT TTT Leu Ile Asn Cys Thr Asp Thr Lys Phe Val Trp Ile Lys Asp Phe 230 235 240	836
AAT ATT TTT GGT AGA GAA TTA AAT GCT ACA GAA GTA TCT TCA CTA TAT Asn Ile Phe Gly Arg Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr 245 250 255	884
TGG ATT CAA TCA TCT ACA AAT ACT TTA AAA GAT TTT TGG GGG AAT CCT Trp Ile Gln Ser Ser Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro 260 265 270 275	932
TTA AGA TAC GAT ACA CAA TAC TAT CTG TTT AAT CAA GGT ATG CAA AAT Leu Arg Tyr Asp Thr Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn 280 285 290	980
ATC TAT ATA AAG TAT TTT AGT AAA GCT TCT ATG GGG GAA ACT GCA CCA Ile Tyr Ile Lys Tyr Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro 295 300 305	1028
CGT ACA AAC TTT AAT AAT GCA GCA ATA AAT TAT CAA AAT TTA TAT CTT Arg Thr Asn Phe Asn Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu 310 315 320	1076
GGT TTA CGA TTT ATT ATA AAA AAA GCA TCA AAT TCT CGG AAT ATA AAT Gly Leu Arg Phe Ile Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn 325 330 335	1124
AAT GAT AAT ATA GTC AGA GAA GGA GAT TAT ATA TAT CTT AAT ATT GAT Asn Asp Asn Ile Val Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp 340 345 350 355	1172
AAT ATT TCT GAT GAA TCT TAC AGA GTA TAT GTT TTG GTG AAT TCT AAA Asn Ile Ser Asp Glu Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys 360 365 370	1220
GAA ATT CAA ACT CAA TTA TTT TTA GCA CCC ATA AAT GAT GAT CCT ACG Glu Ile Gln Thr Gln Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr 375 380 385	1268
TTC TAT GAT GTA CTA CAA ATA AAA AAA TAT TAT GAA AAA ACA ACA TAT Phe Tyr Asp Val Leu Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr 390 395 400	1316
AAT TGT CAG ATA CTT TGC GAA AAA GAT ACT AAA ACA TTT GGG CTG TTT Asn Cys Gln Ile Leu Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe 405 410 415	1364
GGA ATT GGT AAA TTT GTT AAA GAT TAT GGA TAT GTT TGG GAT ACC TAT Gly Ile Gly Lys Phe Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr 420 425 430 435	1412
GAT AAT TAT TTT TGC ATA AGT CAG TGG TAT CTC AGA AGA ATA TCT GAA Asp Asn Tyr Phe Cys Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu 440 445 450	1460

AAT ATA AAT AAA TTA AGG TTG GGA TGT AAT TGG CAA TTC ATT CCC GTG	1508		
Asn Ile Asn Lys Leu Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val			
455	460	465	

GAT GAA GGA TGG ACA GAA TAACTCGAG	1535		
Asp Glu Gly Trp Thr Glu			
470			

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Gly His His His His His His His His Ser Ser Gly His				
1	5	10	15	
Ile Glu Gly Arg His Met Ala Ser Met Ala Asp Thr Ile Leu Ile Gln				
20	25	30		
Val Phe Asn Asn Tyr Ile Ser Asn Ile Ser Ser Asn Ala Ile Leu Ser				
35	40	45		
Leu Ser Tyr Arg Gly Gly Arg Leu Ile Asp Ser Ser Gly Tyr Gly Ala				
50	55	60		
Thr Met Asn Val Gly Ser Asp Val Ile Phe Asn Asp Ile Gly Asn Gly				
65	70	75	80	
Gln Phe Lys Leu Asn Asn Ser Glu Asn Ser Asn Ile Thr Ala His Gln				
85	90	95		
Ser Lys Phe Val Val Tyr Asp Ser Met Phe Asp Asn Phe Ser Ile Asn				
100	105	110		
Phe Trp Val Arg Thr Pro Lys Tyr Asn Asn Asn Asp Ile Gln Thr Tyr				
115	120	125		
Leu Gln Asn Glu Tyr Thr Ile Ile Ser Cys Ile Lys Asn Asp Ser Gly				
130	135	140		
Trp Lys Val Ser Ile Lys Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp				
145	150	155	160	
Val Asn Ala Lys Ser Lys Ser Ile Phe Phe Glu Tyr Ser Ile Lys Asp				
165	170	175		
Asn Ile Ser Asp Tyr Ile Asn Lys Trp Phe Ser Ile Thr Ile Thr Asn				
180	185	190		
Asp Arg Leu Gly Asn Ala Asn Ile Tyr Ile Asn Gly Ser Leu Lys Lys				
195	200	205		
Ser Glu Lys Ile Leu Asn Leu Asp Arg Ile Asn Ser Ser Asn Asp Ile				
210	215	220		

Asp Phe Lys Leu Ile Asn Cys Thr Asp Thr Thr Lys Phe Val Trp Ile  
 225                    230                    235                    240  
 Lys Asp Phe Asn Ile Phe Gly Arg Glu Leu Asn Ala Thr Glu Val Ser  
 245                    250                    255  
 Ser Leu Tyr Trp Ile Gln Ser Ser Thr Asn Thr Leu Lys Asp Phe Trp  
 260                    265                    270  
 Gly Asn Pro Leu Arg Tyr Asp Thr Gln Tyr Tyr Leu Phe Asn Gln Gly  
 275                    280                    285  
 Met Gln Asn Ile Tyr Ile Lys Tyr Phe Ser Lys Ala Ser Met Gly Glu  
 290                    295                    300  
 Thr Ala Pro Arg Thr Asn Phe Asn Asn Ala Ala Ile Asn Tyr Gln Asn  
 305                    310                    315                    320  
 Leu Tyr Leu Gly Leu Arg Phe Ile Ile Lys Lys Ala Ser Asn Ser Arg  
 325                    330                    335  
 Asn Ile Asn Asn Asp Asn Ile Val Arg Glu Gly Asp Tyr Ile Tyr Leu  
 340                    345                    350  
 Asn Ile Asp Asn Ile Ser Asp Glu Ser Tyr Arg Val Tyr Val Leu Val  
 355                    360                    365  
 Asn Ser Lys Glu Ile Gln Thr Gln Leu Phe Leu Ala Pro Ile Asn Asp  
 370                    375                    380  
 Asp Pro Thr Phe Tyr Asp Val Leu Gln Ile Lys Lys Tyr Tyr Glu Lys  
 385                    390                    395                    400  
 Thr Thr Tyr Asn Cys Gln Ile Leu Cys Glu Lys Asp Thr Lys Thr Phe  
 405                    410                    415  
 Gly Leu Phe Gly Ile Gly Lys Phe Val Lys Asp Tyr Gly Tyr Val Trp  
 420                    425                    430  
 Asp Thr Tyr Asp Asn Tyr Phe Cys Ile Ser Gln Trp Tyr Leu Arg Arg  
 435                    440                    445  
 Ile Ser Glu Asn Ile Asn Lys Leu Arg Leu Gly Cys Asn Trp Gln Phe  
 450                    455                    460  
 Ile Pro Val Asp Glu Gly Trp Thr Glu  
 465                    470

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CGCCATGGCT GACACAATT TAAATACAAGT

30

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GCCTCGAGTT ATTCTGTCCA TCCTTCATCC AC

32

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /note= "The asparagine residue at this position contains an amide group."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Cys Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn  
1                   5                   10